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 GGACT 421
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                                                                                                                               GCTGAAGAGGGTGTGCCGGCGCCCCTGCCTCCA-GAGGACGCCCCTAA-CGCCGCATCCC
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This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 1411 'Std Error: 0.00
Seq primer: mob.REGA+ET
High quality segments.
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The WashU Merck EST Project
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4444 Forest Park Parkway, Box 8501, St. Louis,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone_lib="Soares senescent fibroblasts NbHSF"
/tissue_type="senescent fibroblast"
/lab.host="DH10B (ampicillin resistant)"
<1 >443
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/clone="324267"
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No. 0.00e+00;
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                                                                    CGTGACAGCCCACCAACCCCCAACCCTCTACCTCGCAGCCACCCTAAAGGCGACTTCAAG
                                                                                                                                     CGTGACAGCCCAACCAACCCCCAACCCTCTACCTCGCAGCCACCCTAAAGGNGACTTCAAG 123
                                                   AAGATGGAAGGATCTCACGGATCTCATTCCTAATGGTCCGCCGAAGTCTCACACAGTAGA
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: estéwatson.wustl.edu
This Clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 1411 Std Error: 0.00
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WashU-Merck EST Project
Washington University So
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Location/Qualifiers
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llarity 99.5%;
Conservative
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/dbxref="taxon:9806"
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/tlssue_type="senescent fibroblast"
/lab_host="DBHOB (ampicillin resistant)"
complement(<1 >375)
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Pred. No. 0.00e+00;
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GACAGTAAATCAATTTTATTTGTGTTCACAGAANATACTAGGCGATCTCGACAGTCGCTC 63
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488522 3'
AA047184
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Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra, Parsons,J., Rifkin,L., Rohlfing,T., Soares,M.; Tan,F., Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL;
IMAGE Consortium (info@image.llnl.gov) for further i
Seq primer: -40M13 fwd. from Amersham
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4444 Forest park Parkway, Box 8501, St. I
Tel: 314 286 1810
Fax: 314 286 1810
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WashU-Merck EST Project
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Location/Qualifiers
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                               Conservative
                                                                                                           /sex="female"
/dev stage="adult"
/lab_host="DH108"
complement(<1...>35
a 121 c 66 g
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/clone="488522"
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99.7%;
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Pred. No. 0.00e+00;
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Soares,M., Tan,F.,
son,A., Wohldmann,P. and
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Homo sapiens cDNA clone
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                                                                                                                                                                                                                                                                                 BASE COUNT
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                                                               TGTGTTCACAGAACATACTAGGCGATCTCGACAGTCGCTCCGTGACAGCCCACCAACCCC 60
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Ya76f12.s1
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1 (bases 1 to 405)
Hiller,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Tan,F., Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and Wilson,R. Washu-Merck EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                         Email: esr@watson.wustl.edu
Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL, contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Wilson RK
WashU-Merck EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          human clone=67631 library=Stratagene placenta (#937225)
vector=pBluescript SK- host=SOLR cells (kanamycin resistant)
primer=-2ln13 Rsitel=EcoRI Rsite2=EcoRI Rsit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Washington University Scho
4444 Forest Park Parkway,
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no sapiens
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Pred. No. 0.00e+00;
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Bult, C.J., Lee, N.H., Kirkness, E.F., Weinstock, K.G., Gocayne, J.D.,
White, O., Sutton, G., Blake, J.A., Brandon, R.C., Man-Wai, C.,
Clayton, R.A., Cline, T.R., Cotton, M.D., Earle-Hughes, J., Fine, L.D.,
Fitzgerald, L.M., Fitzhugh, W.M., Fritchman, J.L., Geoghagen, N.S.,
Glodek, A., Gnehm, C.L., Hanna, M.C., Hedblom, E., Hinkle, P.S.Jr.,
Kelley, J.M., Kelley, J.C., Liu, L.-I., Marmaros, S.M., Merrick, J.M.,
Moreno-Palanques, R.F., McDonald, L.A., Nguyen, D.T., Pelligrino, S.M.,
Phillips, C.A., Ryder, S.E., Scott, J.L., Saudek, D.M., Shirley, R.,
Small, K.V., Spriggs, T.A., Utterback, T.R., Weidman, J.F., Li, Y.,
Bednarik, D.P., Cao, L., Cepeda, M.A., Coleman, T.A., Collins, E.J.,
Dinke, D., Feng, D.-F., Ferrie, A., Fischer, C., Hudson, P., Kim, A.K.,
Kozak, D.L., Kunsch, C., Hungjun, J., Li, H., Meissner, P.S., Olsen, H.,
Raymond, L., Wei, Y.F., Wing, J., Xu, C., Yu, G.L., Ruben, S.M.,
Dillion, P.J., Fannon, M.R., Rosen, C.A., Haseltine, W.A., Fields, C.,
Fraser, C.M. and Venter, J.C.

Initial assessment of human gene diversity and expression patterns
based upon 83 million nucleotides of CDNA sequence
IAL
96076280
Other T.S. Sutton.
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EST.
                                                                            Email: arkerlav@tigr.org
For clone availability, additional sequence and expression information related to this EST, please check the TIGR Humindex (http://www.tigr.org/tdb/hgi/hgi.html)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
                                                              Seq
                                                                                                                                                                                                                           9712 Medical Center Drive,
                                                                                                                                                                                                                                                                                          Contact: Kerlavage, AR
                                                                                                                                                                                                                                                                                                                 Other_ESTs: THC175266
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2 Medical Center Drive, Rockville,
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                                                                                                             Human Gene
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BASE COUNT
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Best Local S
Matches 36
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783
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                                                                       300 CTNCTTAATTAATNATTTATATGTATTTATGTACGTCCTCCTAAGGTGATGGAGATNTGT
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                                                CTCCT-AATTAAT-ATTTATATGTATTTATGTACGTCCTCCTA-GGTGATGGAGATGTGT
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             ACGTAATATTTATTT
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ACGTAATATTTATTT
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                                                                                                                                                                                                                                                                                                                                                                                                                  105
                                                                                                                                                                                                                                                                                                                                                     Conservative
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EcoRI; Site_2: XhoI"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /db_xref="ATCC (inhost):113941"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                               27.0%;
                       375
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Pred. No. 0.00e+00;
0; Mismatches 7;
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Search completed: Thu Apr 23 05:39:21 1998 Job time : 811 secs.

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Gaps

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Length 475; Indels

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REPLINE; 95.1487.

RA MEDLINE; 95.1487.

RA SCHWIND D.A., JOHNSTON G.I., PAGE S.O., MOSLEY M.J., WILSON K.H.,

RA MORMAN N.P., CAMPBELL S., FIDOCK M.D., FURNESS L.M.,

RA PARRY-SMITH D.J., PETER B., BAILEY D.S.;

RI PHARMACOL. EXP. THER. 272:134-142(1995)

C. I. PHARMACOL. EXP. THER. 272:134-142(1995)

C. I. FUNCTION WITH G. PROTEINS THAT ACTIVATE A PHOSPHATIDYLINOSITOL-

C. CALCIUM SECOND MESSENGER SYSTEM.

C. SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.

C. SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.

C. SUBCELLULAR LOCATION: OF FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.

EMBL; M99589; -; NOT_ANNOTATED_CDS.

EMBL; M99590; -; NOT_ANNOTATED_CDS.

EMBL; M99590; -; NOT_ANNOTATED_CDS.

EMBL; M99511; A45121.

DR PIR; A45121, A45121.

CROBB; GCR.0530; -.
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Best Local Similarity 28.6%;
Matches 18; Conservative
                                                                                                      TRANSMEM
DOMAIN
TRANSMEM
DOMAIN
           TRANSMEM
DOMAIN
TRANSMEM
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TRANSMEM
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DOMAIN
                                                                                                                                                            MULTIGENE
DOMAIN
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LEPOR H., HARTIG P.R.,
GLUCHOWSKI C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-JUN-1994 (REL. 29, CREATED)
01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)
01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)
ALPHA-1B ADRENERGIC RECEPTOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A1AB_HUMAN
P35368;
                                                                                                                                                                                                 MIM; 104220; -. PROSITE; PS00237;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
MEDLINE; 93016158.
RAMARAO C.S., DENKER J.M., PEREZ D.M., GAIVIN R.J., RIEK R.P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HOMO SAPIENS (HUMAN).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
                                                                                                                                                                                        G-PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOL. PHARMACOL. 45:703-708(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE-BRAIN;
MEDLINE; 94239386.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GRAHAM R.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EUTHERIA; PRIMATES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             358 LICPILFDKVTTDMRLAWEE-PFGPVLPIIRVTSVEEAIEISNK-SEYGLQASIFTNDFP 415
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BIOL. CHEM. 267:21936-21945(1992).
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                                                                                                                                                                         COUPLED FAMILY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BARD J.A., WETZEL J.M., CHIU G., SHAPIRO E., TANG R., JARTIG P.R., WEINSHANK R.L., BRANCHEK T.A.,
 1
46
71
106
116
1142
142
183
202
202
203
203
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                                                                                                                                             RECEPTOR: TRANSMEMBRANE; GLYCOPROTEIN; PHOSPHORYLATION; LIPOPROTEIN; PALMITATE. 45 EXTRACELLULAR (POTENTIAL). 70 1 (POTENTIAL).
                                                                                                                                                                                                   G_PROTEIN_RECEPTOR; 1
 45
70
105
115
141
141
161
182
201
201
329
329
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Pred. No. 6.05e-01
19; Mismatches 2
                                                4 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
                                                                                                      EXTRACELLULAR (POTENTIAL)
                                                                                                                     CYTOPLASMIC (
2 (POTENTIAL)
               CYTOPLASMIC
6 (POTENTIAL
                                                                              CYTOPLASMIC
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EXTRACELLULAR (POTENTIAL)
                                                                                          (POTENTIAL)
             (POTENTIAL
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                                                                           (POTENTIAL).
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CARBOHYD
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         451 ALLSLPAPEPPGRRG-RHDSGP-LFTFKLLTEPES-PGTDGGASNG 493
12 TILQAPTPAPSTIPGPRRGSGPEIFTFDPLPEPAAAPAGRPSASRG 57
                           8.8%;
Similarity 41.3%;
19; Conservation
                                                            327
341
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POTENTIAL.

POTENTIAL.

BY SIMILARITY.

BY SIMILARITY.

PALMITATE (POTENTIAL).

MISSING (IN REF. 1).

AAAD -> PRH (IN REF. 1).

AAAD -> RG (IN REF. 2).

MY; D088058C CRC32;
                                      Score 98; DB 1;
Pred. No. 6.05e-01
                                                                                                                                      7 (POTENTIAL)
CYTOPLASMIC (I
POLY-ARG.
                               9,
                               Mismatches
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Best Local
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01-JUL-1993
01-NOV-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    JINDEBERG M., COLLMER A.;
J. BACTERIOL. 174:7385-7397(1992).
I. FUNCTION: INVOLVED IN A GENERAL SECRETION PATHWAY EXPORT OF PROTEINS. REQUIRED FOR THE TRANSLOCATION MULTIPLE PECTIC ENZYMES.
I. SUBCELLULAR LOCATION: INNER MEMBRANE (PROBABLE).
I. SIMILARITY: BELONGS TO THE EXEC/PULC/OUTC FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                               GENERAL OUTC).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DOMAIN
SEQUENCE
                                                                                                                                  DOMAIN
SEQUENCE
                                                                                                                                                                                                                                              MEDLINE; 93086427.

CONDEMINE G., DOREL C., HUGOUVIEUX-COTTE-PATTAT N., ROBERT-BAUDOUY J.;

MOL. MICROBIOL. 6:3199-3211(1992).

-!- FUNCTION: INVOLVED IN A GENERAL SECRETION PATHWAY (GSP) FOR THE

EXPORT OF PROTEINS. REQUIRED FOR THE TRANSLOCATION OF THE

MULTIPLE PECTIC ENZYMES.
                                                                                                                                                                                                                        -!- SUBCELLULAR LOCATION: INNER
-!- SIMILARITY: BELONGS TO THE
                                                                                                                                                                                                                                                                                                        STRAIN-3937
MEDLINE; 93
                                                                                                                                                                                                                                                                                                                                                              ERWINIA CHRYSANTHEMI. PROKARYOTA; GRACILICUTES;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE; PS01141; T2SP_C; TRANSPORT; TRANSMEMBRANE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE; 93054355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-EC
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                                                                                                                                                                                         PIR; S28013; S28013.
PROSITE; PS01141; T2SP_C;
                                                                                                                                                                                                                 EMBL;
                                                                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                     ENTEROBACTERIACEAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                      001564;
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VGLI_HSV11
                                                                                                                                                                    DOMAIN
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                                                                 6 LPPLSPSVIRRILFYLLMLLFCQQL-AMIFWRIGLP-DNAP-VSSVQITPAQARQQPVTL 62
           13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LPPLSPSVIRRILFYLLMLLFCQQL-AMIFWRVGLP-DNSP-VASVQITPAQARQQPVTL 62
                                            LPVEEPNPAKRLLFLLLTIVFCQILMAEEGVPAPLPPEDAPNAASLAPTPVSPVLEPFNL 134
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22; Conser
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22; Conse
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36
272
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36
272
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1 16 CYTOPLASMIC (POTENTIAL).
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(REL.
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larity 36.7%;
Conservative
                                                                                      8.8%;
larity 36.7%;
Conservative
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26. LAST SEQUENCE UPDATE)
32. LAST ANNOTATION UPDATE)
PATHWAY PROTEIN C (PECTIC ENZYMES
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35
272
30301
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30162
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X
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CYTOPLASMIC
POTENTIAL.
                                                                                                                                                                                                                          INNER MEMBRANE (PROBABLE).
O THE EXEC/PULC/OUTC FAMILY
                                                                                                                                    W.
                                                                                                                                                                                                                                                                                                                                                               SCOTOBACTERIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 99;
Pred. No.
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11; 1
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Pred.
11; M
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PERIPLASMIC (POTENTIAL).
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7944F46D C
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PRT;
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1. NO. 4.56e-01;
Mismatches: 24
                                                                                      re 98; DB 1; 1
1. No. 6.05e-01
Mismatches 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                272
 390
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                                                                                        24;
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                                                                                                           Length 272
                                                                                                                                                                                                                           FAMILY
                                                                                       Indels
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STATE DESCRIPTION OF THE WARRANT COCCURATE T
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Best Local Similarity
Matches 25; Conser
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EMBL; L10036; G29147; -.
EMBL; X14112; G59565; -.
EMBL; X02138; G59879; -.
PIR; A05243; QQBE77.
OXIDOREDUCTASE;
NP_BIND 230
ACT_SITE 250
ACT_SITE 284
SEQUENCE 475 A
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CARBOHYD
CARBOHYD
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01-JAN-1988
01-JAN-1988
01-OCT-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-NOV-1997 (REL. 35, CREATED)
01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
NADP-DEPENDENT GLYCERALDEHYDE-3-PHOSPHATE DEHYDROGENASE (EC 1.2.1.
(NON-PHOSPHORYLATING GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE)
(GLYCERALDEHYDE-3-PHOSPHATE DEHYDROGENASE (NADP+)) (TRIOSEPHOSPHAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MCGEOCH D.J., DOLAN A., DONALD S., RIXON F.J.;
J. MOL. BIOL. 181:1-13(1985).
J. THERE ARE SEVEN EXTERNAL GLYCOPROTEINS IN HSV1 AN
GG, GD, GI, AND GE.
J. SIMILARITY: TO OTHER HERPESVIRUSES GLYCOPROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GLYCOPROTEIN
GI OR US7.
                                                                                                                                                 EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q59931;
01-NOV-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. MEDLINE; 85160822.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HERPES SIMPLEX VIRUS (TYPE 1 / VIRIDAE; DS-DNA ENVELOPED VIRUS
                                                                                                                                                                                                                                                  BOYD D.A., CVITKOVITCH D.G., HAMILTON J. BACTERIOL. 177:2622-2627(1995).
-!- FUNCTION: IMPORTANT AS A MEANS OF
                                                                                                                                                                                                                                                                                                                     STRAIN-NG5 SEROTYPE C;
MEDLINE; 95270576.
                                                                                                                                                                                                                                                                                                                                                                                                         STREPTOCOCCUS MUTANS. PROKARYOTA; FIRMICUTES;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GAPN_STRMU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GLYCOPROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         GAPN
                                                                                                       PROSITE; PS00070; ALDEHYDE_DEHYDR_CYS; PROSITE; PS00687; ALDEHYDE_DEHYDR_GLU;
                                                                                                                                                                     -!- SIMILARITY: BELONGS
                                                                                                                                                                                                             BIOSYNTHETIC REACTIONS.
-I- CATALYTIC ACTIVITY: D-GLYCERALDEHYDE
                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DEHYDROGENASE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        206 QASTPSTTTSTPSTTIPAPSTTIPAPQASTTP-FPTGDPKPQPPGVNHEPPSNA-TRATR 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          264 DSR--YALTVTQIIQIAIPASIIALVFL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    w
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SRRVLYPRVVRRQLPVEEPNPAKRLLFL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HSRSCHPTMTILQAPTPAPST-IPGPRRGSGPEIFTFDPLPEPAAAPAGRPSASRGHRKR
                                                                                                                                                 L38521; G642667;
                                                                                                                                                                                           3-PHOSPHO-D-GLYCERATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       390 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (REL.
(REL.
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175
257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
    AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                      NADP
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34,
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175
257
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    51221
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LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDAT
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    WW;
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VIRUSES; HEI
                                                                                                                                                                     THE ALDEHYDE DEHYDROGENASES FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 98; DB 1;
Pred. No. 6.05e-01
21; Mismatches 3
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POTENTIAL.
                   NAD (ADP PART) (BY
BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                             STREPTOCOCCAEAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7DA38E2D CRC32;
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HERPESVIRIDAE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                475
                                                                                                                                                                                                                                                                                                   I.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  UPDATE)
                                                                                                                                                                                                                                                         GENERATING
                                                                                                   1.
FALSE_NEG
                                                                                                                                                                                                               3-PHOSPHATE + NADP(+)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               390;
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
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KAGEYAMA R., SASAI Y., NAKANISHI S.;

KAGEYAMA R., SASAI Y., NAKANISHI S.;

J. BIOL. CHEM. 266:15525-15531(1991).

-i- FUNCTION: C/EBP IS A DNA-BINDING PROTEIN THAT RECOGNIZES TWO DIFFERENT MOTIFS: THE CCAAT HOMOLOGY COMMON TO MANY PROMOTERS.

THE ENHANCED CORE HOMOLOGY COMMON TO MANY ENHANCERS.

-i- SUBUNIT: BINDS DNA AS A DIMER.

-i- SUBCELLULAR LOCATION: NUCLEAR.

-i- TISSUE SPECIFICITY: UBICUTTOUSLY EXPRESSED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DNA_BIND
                                                                                                                                                                   NON_TER
                                                                                             TRANSMEM
DOMAIN
                                                                                                                                                                                                             GCRDB; GCR_0017; -.

PROSITE; PS00237; G_PROTEIN_RECEPTOR; 1.

G-PROTEIN COUPLED RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN;
MULTIGENE FAMILY; PHOSPHORYLATION; LIPOPROTEIN; PALMITATE.
                                                                                                                                                                                                                                                                                                                              -!- SUBCELLULAR LOCATION:
-!- SIMILARITY: BELONGS TO
EMBL; X14050; G833784; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LIBERT F., PARMENTIER M., LEFORT A., MAENHAUT C., SIMONS M.-J., DUMONT J. SCIENCE 244:569-572(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Alab_Canfa STANDARD; PRT; 417 AA. P11615; 01-0CT-1989 (REL. 12, CREATED) 01-0CT-1989 (REL. 12, LAST SEQUENCE UPDATE) 01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL;
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RATTUS NORVEGICUS (RAT).

EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE; 89242119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE-THYROID;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EUKARYOTA; METAZOA;
EUTHERIA; CARNIVORA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADRA1B OR RDC5.
CANIS FAMILIARIS (DOG)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TRANSCRIPTION REGULATION; ACT:
DNA_BIND 197 215 I
DOMAIN 226 254
SEQUENCE 268 AA; 28600 MW;
                                                                                                                                            DOMAIN
                                                                                                                                                                                                                                                                                                             PIR; E30341; E30341.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ALPHA-1B ADRENERGIC RECEPTOR (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TRANSFAC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE-BRAIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
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                                                 DOMAIN
                                                                          TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                            -!- FUNCTION: THIS ALPHA-ADRENERGIC RECEPTOR N
ASSOCIATION WITH G PROTEINS THAT ACTIVATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      142 CAQTVVSLAAAAQPTPPTSPEPPRGSPGPSLAP-GPVREKGAGKRGPDRGSPEYRQRRER 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
les 22; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7
                                                                                                                                                                                                                                                                                                                                                     CALCIUM SECOND MESSENGER SYSTEM.
SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CHPTMTILOAPT-PAPSTIPGPRRGS-GPEIFTEDPLPEPAAAPAGRPSASRGHRKRSRR 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 B39429; B39429.
SFAC; T00109; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                M65149; G203412; -.
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45
45
105
128
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9.1%;
  8
20
44
64
85
104
127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CHORDATA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ACTIVATOR; DNA-BINDING; BASIC MOTIF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 101; DB 1;
Pred. No. 2.57e-01;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10;
4 (POTENTIAL).

EXTRACELLULAR (POTENTIAL)

5 (POTENTIAL).

CYTOPLASMIC (POTENTIAL).
                                                                     EXTRACELLULAR (POTENTIAL).
3 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
4 (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LEUCINE-ZIPPER
                                                                                                                                                                   N
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                                                                                                                                                                   (POTENTIAL)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  , DINSART C., VAN SANDE
                                                                                                                                                                                                                                                                                                                                                          G-PROTEIN COUPLED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TETRAPODA; MAMMALIA;
                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIATES ITS ACTION BY E A PHOSPHATIDYLINOSITOL-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length
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Best Local S
Matches 1
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Best Local S
Matches
                                            GSPC_ERWCH STAN
P31698;
01-JUL-1993 (REL. 2
01-JUL-1993 (REL. 2
01-NOV-1995 (REL. 3
GENERAL SECRETION F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OAIF_NEUCR
QAIF_NEUCR
P11638;
P1-0CT-1989
01-0CT-1989
01-0CT-1989
                       GENERAL OUTC).
                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.

STRAIN-74-0R23-1A;

MEDLINE; 89293848.

MEDLINE; 89293848.

GEBYER R.F., HUIET L., BAUM J.A., TYLER B.M., PATEL V.B.,

GEBYER B.J., CASE M.E., GILES N.H.;

J. MOL. BIOL. 207:15-34(1989).

-!- FUNCTION: TRANSCRIPTION ACTIVATION OF GENES FOR ENZYMES AND
PROTEINS OF QUINATE METABOLISM BY BINDING TO A 16 BASE-PAIR
SEQUENCE (CONSENSUS GGRTAARYRYTTAYCC) IN FRONT OF EACH QA GE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TRANSMEM
DOMAIN
TRANSMEM
DOMAIN
DOMAIN
DOMAIN
DISULFID
LIPID
                                                                                                                                                                                                                                               PROSITE; PS00463; ZN2_CY6_FUNGAL_1; 1.

PROSITE; PS50048; ZN2_CY6_FUNGAL_2; 1.

TRANSCRIPTION REGULATION; ACTIVACE, DNA-BINDING; NUCLEAR ZINC; METAL-BINDING; QUINATE METABOLISM.

DNA_BIND 76 103 ZN(2)-CYS(6), FUNGAL-TYPE. METABOLISM.

DOMAIN 773 793 ASP/GLU-RICH (ACIDIC).

SEQUENCE 816 AA; 88946 MW; E99EACA7 CRC32;
ERWINIA CHRYSANTHEMI. PROKARYOTA; GRACILICUTES;
                                                                                                                                                                                                                                                                                                                                  EMBL; X14603; G3068; -. PIR; S04256; S04256. PIR; F31277; F31277. TRANSFAC; T00709; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NEUROSPORA CRASSA.
EUKARYOTA; FUNGI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QUINIC ACID QA-1F.
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                                                                                                                                                                             408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  353 ALLSLPAPQPPGRRG-RRDSGP-LFTFRLLAERGSPAAG 389
                                                                                                                                                    70 VVRRQLPVEEPNPAKRLLFLLTIVFCQILMA-EEGVPAPLPPEDAPN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12 TILQAPTPAPSTIPGPRRGSGPEIFTFDPLPEPAAAPAG
                                                                                                                                                                                                                                                                                                                                                                                 SUBCELLULAR LOCATION: NUCLEAR.
SIMILARITY: CONTAINS A ZN(2)-CYS(6), FUNGAL-TYPE BINUCLEAR
CLUSTER DOMAIN.
                                                                                                                                                                           VVRTQLPPDDDRPRPRMRALLVACFIVDTIVSMRHNVPAHLKPDDIAD
                                                                                                                                                                                                     Similarity
16; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                268
417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (REL. 12, CREATED)
(REL. 13, LAST SEQUENCE UPDATE)
(REL. 23, LAST ANNOTATION UPDAT
UTILIZATION ACTIVATOR.
                                                                                                                                                                                                  9.1%;
larity 33.3%;
Conservative
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                                                                                                        STANDARD;
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229
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                                             26, CREATED)
26, LAST SEQUENCE UPDATE)
32, LAST ANNOTATION UPDAT
PATHWAY PROTEIN C (PECTIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ASCOMYCOTINA;
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SCOTOBACTERIA;
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                                                                                                                                                                                                  Score 101; DB 1;
Pred. No. 2.57e-01;
13; Mismatches 18
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Pred. No. 2.57e-01;
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PALMITATE (POTENTIAL)
; 8008E9B3 CRC32;
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BY SIMILA
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EXTRACELLULAR (POTENTIAL).
7 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PYRENOMYCETES;
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                                               (PECTIC
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 FACULTATIVELY
                                               ENZYMES
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                                               SECRETION
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 ANAEROBIC RODS
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Matches
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                                                                                                                                                                                                       MEDLINE; 92112033.

GRUSSBY-JACKSON L., KUO A., LEDER P.;
GRUSSBY-U 6:29-37(1992).

-i- FUNCTION: IS IMPORTANT IN THE MORPHOGENESIS OF LIMB AND MAY HAVE A FUNCTION IN DIFFERENTIATED CELLS OR BE INVOLVED IN MAINTAINING SPECIFIC DIFFERENTIATED STATES.

-1- TISSUE SPECIFICITY: IT IS FOUND THROUGHOUT THE EMBRYO BUT HAS A FUNCTIONAL ROLE ONLY IN THE KIDNEY AND LIMB.
-1- DEVELOPMENTAL STAGE: THIS IS THE ISOFORM FOUND IN THE APICAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M.,
BONFIELD J., BURTON J., CONNELL M., COPSEY T., COOPER J., COULSON A
CRAXTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FRASER A.,
FULTON L., GARDNER A., GREEN P., HAWKINS T., HILLIER L., JIER M.,
JOHNSTON L., JONES M., KERSHAW J., KIRSTEN J., LAISSTER N.,
LATREILLE P., LIGHTNING J., LLOYD C., MORTIMORE B., O'CALLAGHAN M.,
LATREILLE P., LIGHTNING J., LLOYD C., MORTIMORE B., O'CALLAGHAN M.,
PARSONS J., PERCY C., RITKEN L., ROOPRA A., SAUNDERS D., STADEN R.,
SULSTON J., THIERRY-MIEG J., THOMAS K., VAUGIN M., VAUGHAN K.,
RITHERRY-MIEG J., THOMAS K., VAUGIN M., VAUGHAN K.,
RITHERRY-MIEG J., THOMAS K., VAUGIN M., VAUGHAN K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WOHLDMAN P.;
NATURE 368:32-38(1994).
EMBL; L16621; G289783; -.
PIR; S44920; S44920.
                                                                                 EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       MUS MUSCULUS (MOUSE).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; RODENTIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-JUN-1994 (REL
01-JUN-1994 (REL
01-FEB-1995 (REL
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                                                 PIR; S24407; S24407.
HSSP; P19999; 1CLG.
                                                                                                                                                                                           -
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                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 205859;
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                DOMAIN
                                    NUCLEAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        962
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                                                                                                                ALTERNATIVE PRODUCTS: MANY DIFFERENT FORMS OF THIS PROTEIN ARE PRODUCED BY ALTERNATIVE SPLICING OF THE LD GENE. A VARIATION IN SPLICING IS SEEN AMONG DIFFERENT TISSUES AND DIFFERENT SIZE TRANSCRIPTS EXIST WITHIN ANY ONE TISSUE. THIS IS ISOFORM 4 AND IDIFFERENT IN ITS N-TERMINAL TO THE OTHER MOUSE ISOFORMS SO FAR
                                                                                                     DETERMINED
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ILQAPTPAPSTIPGPRRGSGPEIFTFDPLPEPAAAPAGR-PSASRGHRKRSRRVLYPRVV 71
PROTEIN; DEVELOPMENTAL PROTEIN; 635 638 POLY-SER. 644 744 PRO-RICH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  h 9.8%;
Similarity 23.7%;
31; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R., WATSON A., WEINSTOCK L., WILKINSON-SPROAT J.,
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                                                                                 G51553;
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EL. 29, LAST SEQUENCE UPDATE)
EL. 31, LAST ANNOTATION UPDATE)
DEFORMITY PROTEIN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
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Pred. No. 2.43e-02;
30; Mismatches 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
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                                ALTERNATIVE SPLICING
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Best Local Similarity 39.1%;
Matches 18; Conservative
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                CEBD_RAT STAN
Q03484;
01-OCT-1996 (REL. 3
01-OCT-1996 (REL. 3
01-NOV-1997 (REL. 3
CCAAT/ENHANCER BIND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DOMAIN
SEQUENCE
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Q05860;
                                                                                                                                                                                                                                                                                                                                                                                                 DOMAIN
DOMAIN
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PIR; S1
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WOYCHIK R.P., MAAS R.L.,
NATURE 346:850-853(1990)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-JUN-1994 (REL. 29, CREATED)
01-JUN-1994 (REL. 29, LAST SEQUENCE UP
01-NOV-1997 (REL. 35, LAST ANNOTATION
FORMIN (LIMB DEFORMITY PROTEIN).
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EUKARYOTA; METAZOA; CHORDATA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FMN OR LD.
                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
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MGD; MGI:101815; FMN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HSSP; P19999;
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                                                                                                                                                                                                                                                                                                                                                                                   DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUCLEAR
                                                                                                                                                                                                                    942 VLALPNSGGPPP-PPPPPPPPPPPPPPPPPPPP-PPGL-SFGLSSSSQYP 984
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SUBCELLULAR LOCATION: NUCLEAR.

TISSUE SPECIFICITY: IT IS PRESENT IN THE ADULT KIDNEY, TESTIS, LIMB, OVARY, BRAIL, SMALL INTESTINE, SALIVARY GLAND AND HARDERIAN GLAND. IT IS PRESENT THROUGHOUT THE EMBRYO.

DEVELOPMENTAL STAGE: IN THE DEVELOPING LIMB BUD, THE PROTEIN IS EXPRESSED IN THE APICAL ECTODERWAL RIDGE AND THE MESENCHYMAL COMPARTMENT, PREDOMINANTLY IN THE POSTERIOR REGION. DURING KIDNEY MORPHOGENESIS, EXPRESSION IS INITIALLY RESTRICTED TO THE EPITHELIAL COMPARTMENT OF THE PRONEPHROS. AND MESONCEPHROS.

ALTERNATIVE PRODUCTS: MANY DIFFERENT FORMS OF THE LD GENE. A VARLATION IN SPLICING IS SEEN AMONG DIFFERENT TISSUES AND ARE PRODUCED BY ALTERNATIVE SPLICING OF THE LD GENE. A VARLATION IN SPLICING IS SEEN AMONG DIFFERENT TISSUES AND DESCRIPTION AND ONE TISSUES AND CARRATTOR THE PROPERTY OF THE LD GENE. A VARLATION IN SPLICING IS SEEN AMONG DIFFERENT TISSUES AND DESCRIPTION AND ONE TISSUES AND CARRATTOR STATE THE ADMINISTRATION OF THE METHOR AND ONE TISSUES AND DESCRIPTION AND ONE TISSUES AND THE TISSUES
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L; X53599; G52878;
; S11515; S11515.
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                                                                                                                                                                                                 IL-MAEEGVPAPLPPEDAPNAASLAPTPVSPVLEPFNLTSEPSDYA 142
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18; Conser
                                                                                                                                                                                                                                                                                                                                                                               PROTEIN; DEVELOPMENTAL PROTEIN;
298 301 POLY-SER.
861 864 POLY-SER.
869 970 PRO-RICH.
977 981 POLY-SER.
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1206
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larity 39.1%;
Conservative
                  REL. 34, C
REL. 34, I
REL. 35, I
R BINDING
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                                                                                                                      STANDARD;
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LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
G PROTEIN DELTA (C/EBP D
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                                                                                                                                                                                                                                                                                                                                                              MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 103; DB 1;
Pred. No. 1.44e-01
15; Mismatches
                                                                                                                                                                                                                                                                             Score 103; DB 1;
Pred. No. 1.44e-01;
15; Mismatches 9
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                                                                                                                      PRT;
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                                                                                                                      268
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                    DELTA)
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                                                                                                                                                                                                                                                                                                                      Length 1468;
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                  Matches
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CHARLES C.H., YOON J.K., SIMSKE J.S., LAU L.F.;

ONCOGENE 8:797-801(1993).

-I- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN (POTENTIAL).

-I- TISSUE SPECIFICITY: EXPRESSED PREDOMINANTLY IN THE LUNG, T.

AND THE UTERUS.

-I- INDUCTION: BY SERUM GROWTH FACTORS.
                                                                                                                                                                                                                                                                                                                                                                                                 DOMAIN
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-NOV-1995 (REL. 32, CREATED)
01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)
01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
01-NOV-1997 (REL. 35, LAST AÑNOTATION UPDATE)
RADIATION-INDUCIBLE IMMEDIATE EARLY GENE IEX-1 (IMMEDIATE
PROTEIN GLY96) (IMMEDIATE EARLY RESPONSE 3 PROTEIN).
IEX1 OR GLY96 OR IER3.
MUS MUSCULUS (MOUSE).
EUXARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMA
                                             01-NOV-1990 (REL. 16, CREATED)
01-NOV-1990 (REL. 16, LAST SEQUENCE UP
01-FEB-1991 (REL. 17, LAST ANNOTATION
VIRAL PROTEIN TPX.
THERMOPROTEUS TENAX VIRUS 1 (STRAIN VI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -!- INCOCATOR GLYCOSYLATED.
-!- PTM: GLYCOSYLATED.
-!- SIMILARITY: STRONG, TO HUMAN OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
STRAIN=BALB/C;
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P46694;
                                                                                                               VTP3_TTV1V
P19275;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  GLYCOPROTEIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             PIR; S33363; S33363.
MGD; MGI:104814; IER3.
SEQUENCE FROM N.A. MEDLINE; 90245666.
                                     THERMOPROTEUS TENAX VIRUS 1 (STRAIN VT3) (TTV1).
VIRIDAE: DS-DNA ENVELOPED VIRUSES: LIPOTHRIXVIRIDAE.
                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                       DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                           TRANSMEM
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                                                                                                                                                                                                                                                                                           1 MCHSRNHLHTMTGLRAPSPAPSTGPELRRGSGPEIFTFDPLPERAVVSTARLNTSRGHRK
                                                                                                                                                                                          EPISAPITAPPVLEPLNLTSESSDYALDLKAFL 153
                                                                                                                                                                           | :|:: |||||:|||||:|||||| :||
AP--TPVS--PVLEPFNLTSEPSDYALDLSTFL 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOUSE
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                                                                                                                                                                                                                             RSRRVLYPRVVRRQLPVEEPNPAKRLLFLLLTIVFCQILMAEEGVPAPLPPEDAPNAASL
                                                                                                                                                                                                                                                                              MCHSRSCHPTMTILQAPTPAPSTIPGPRRGSGPEIFTFDPLPEPAAAPAGRPSASRGHRK
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103
137
153 AA;
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larity 70.6%;
Conservative
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                                                                                                                           STANDARD;
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102
153
137
                                                                                                                                                                                                                                                                                                                                                                                     16875 MW;
                                                                                                                                                                                                                                                                                                                              Score 752; DB 1; I
Pred. No. 1.15e-120;
22; Mismatches 19;
                                                                                                                                                                                                                                                                                                                                                                                 CYTOPLASMIC (POTENTIAL).
POTENTIAL.
EXTRACELLULAR (POTENTIAL).
POTENTIAL.
7A284EC2 CRC32;
                                                                                                                          PRT;
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                                                                                     UPDATE)
                                                                                                                          474
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                                                                         UPDATE)
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SEQUENCE FROM N.A.
MEISSNER J.D., HIRSCH G.N., LARUJ
SUBMITTED (MAX'-1997) TO EMBL/GEN
EMBL; U95843; G2072333; -
CORE PROTEIN; LATE PROTEIN.
SPOJTENCE 228 AA; 25571 MW; I
                                 NEUMANN H., ZILLIG W.;
NUCLEIC ACIDS RES. 18:2
EMBL; X14717; E20711; -
PIR; S06686; S06686.
PIR; S15921; S15921.
                                                                                                                                                                                                                                                                                                                                                                            010442:
01-NOV-1997 (REL. 35, CREATED)
01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
01-NOV-1997 (REL. 35, LAST ANNOTATION UPDAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REPEAT
SEQUENCE
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REPEAT
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VIRIDAE; DS-DNA NONENVELOPED VIRUSES; ADENOVIRIDAE;
                                                                                                                                                                                                                                                                                                                                                                      MINOR CORE PROTEIN (PROTEIN V).
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nes 27; Conser
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                                                                                                                                                                        VERRRRVAQTVPVVRYHPSIQVEPAVHPPLAP 212
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                                                                                                                                                      NPAKRLLFLLLTIV-FCQILMAEEGVPAPLPP
                                                                                                                                                                                           PSTIPGPRRGSGPEIFTFDPLPEPAAAPAGRPSASRGHRKRSRRVLYPRVVRRQLPVEEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                           RVVRRQLPVEEPNPAKRLLFLLLTIVFCQILMAEEGVPAPLPPEDAPNAASLAPTPVS 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TPTPTPTPTPTPTPTPTYDITYVVF-DVTPSPTPTPTPTPTPTPTPTPTPTPTPTPTP 405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       h 10.5%;
Similarity 23.7%;
28; Conservative
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ilarity 29.3%;
Conservative
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368
378
437
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377
436
446
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                                                                                                                                                                                                                                                                                                    H G.N., LARUE E.A., FULCHER R.A., TO EMBL/GENBANK/DDBJ DATA BANKS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MW;
                                                                                                                                                                                                                                Score 112; DB 1;
Pred. No. 9.76e-03;
21; Mismatches 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 117; DB 1;
Pred. No. 2.07e-03;
26; Mismatches 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               THR-PRO(N)
BAC5D831
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3 THR-PRO REPEATS REGIONS AND TWO NEAR IDENTICAL REPEATS.
THR-PRO(N).
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                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
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                                                                                                                                                                                                                                 Mismatches 41;
                                                                                                                                                                                                                                                                                                                                                                                                                       228
                                                                                                                                                      111
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                                                                                                                                                                                                                                                                                                             SPINDLER K.R.;
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                                                                                                                                                                                                                                 Gaps
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SEQUENCE FROM N.A. STRAIN-BRISTOL N2; MEDLINE; 94150718.

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rch_pp protein - protein database search, using Smith-Waterman algorithm

Tabular output not generated. Fri Apr 17 13:38:32 1998; MasPar time 6.24 Seconds 626.917 Million cell updates/sec

Title:

Description: Perfect Score: Sequence: >US-08-799-910-10 (1-156) from US08799910.pep 1114 1 MCHSRSCHPIMTILQAPIPA.....EPSDYALDLSTFLQQHPAAF 156

Scoring table:

PAM 150 Gap 11

Searched: 69112 seqs, 25083644 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database: swiss-prot35 1:swiss1

Statistics: Mean 44.412; Variance 91.621; scale 0.485

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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22	270	19	18	17	16	15	14	13	12	11	10	9	œ	7	თ	υ	4	ω	N	_	No.
956	9 6 9 9	97	97	97	98	98	98	98	98	99	101	101	101	103	103	109	112	117	752	1102	Score
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1233	245	1337	1239	1043	975	519	475	390	272	272	816		268	1468	1206	1799	228	474	153	156	Length
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NME3_HUMAN	VE4_HPV5B	PTPJ_HUMAN	V120_EBV	CHS2_PARBR	CDP_CANFA	Alab_HUMAN	GAPN_STRMU	VGLI_HSV11	GSQC_ERWCH	GSPC_ERWCH	QA1F_NEUCR	A1AB_CANFA	CEBD_RAT	FORM_MOUSE	FOR4_MOUSE	YO25_CAEEL	VCOM_ADEM1	VTP3_TTV1V	IEX1_MOUSE	IEX1_HUMAN	ID
S. C.	PROBABLE E4 PROTEIN.	N-TYROSINE	ASSEMBLY PR	CHITIN SYNTHASE 2 (EC	CCAAT DISPLACEMENT PRO	ALPHA-1B ADRENERGIC RE	NADP-DEPENDENT GLYCERA	GLYCOPROTEIN I.	GENERAL SECRETION PATH	GENERAL SECRETION PATH	QUINIC ACID UTILIZATIO	ALPHA-1B ADRENERGIC RE	CCAAT/ENHANCER BINDING	FORMIN (LIMB DEFORMITY	O		MINOR CORE PROTEIN (PR	VIRAL PROTEIN TPX.	RADIATION-INDUCIBLE IM	RADIATION-INDUCIBLE IM	Description
1.06e+00	1.06e+00	8.02e-01	8.02e-01	8.02e-01	6.05e-01	6.05e-01	6.05e-01	6.05e-01	6.05e-01	4.56e-01	2.57e-01		2.57e-01	1.44e-01	1.44e-01	2.43e-02	9.76e-03	2.07e-03	1.15e-120	5.97e-191	Pred. No.

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45	44	43	42	41	40	39	38	37	36	ω 5	34	33	32	31	30	29	28	27	26	25	24
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440	1692	926	820	631	620	517	464	350	276	268	232	1742	389	279	217	3866	643	534	493	449	316
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YW19_MYCTU	POLN_HEVPA	YIK9_YEAST	FIBL_HUMAN	DMK_MOUSE	EXTN_TOBAC	MBEA_ECOLI	SP62_HUMAN	Y08N_MYCTU	YIT4_YEAST	CEBD_MOUSE	SAX1_CHICK	GUNA_CALSA	NDPP_MOUSE	Y091_NPVOP	YKR4_EBV	HRX_MOUSE	VP40_HSVE2	APG_ARATH	GUNA_XANCP	APG_BRANA	CDNC_HUMAN
HYPOTHETICAL 45.3 KD T	NON-STRUCTURAL POLYPRO	HYPOTHETICAL 103.6 KD	FIBRINOGEN-LIKE PROTEI	MYOTONIN-PROTEIN KINAS	EXTENSIN PRECURSOR (CE	MOBILIZATION PROTEIN M	SPLICEOSOME ASSOCIATED	HYPOTHETICAL 37.0 KD P	HYPOTHETICAL 31.3 KD P	CCAAT/ENHANCER BINDING	HOMEOBOX PROTEIN SAX-1	ENDOGLUCANASE A PRECUR	NPC DERIVED PROLINE RI	HYPOTHETICAL 29.3 KD P	HYPOTHETICAL BKRF4 PRO	z	CAPSID PROTEIN P40 (CO	ANTER-SPECIFIC PROLINE	MAJOR EXTRACELLULAR EN	ANTER-SPECIFIC PROLINE	CYCLIN-DEPENDENT KINAS
4.15e+00	3.17e+00	3.17e+00	3.17e+00	3.17e+00	3.17e+00	2.42e+00	2.42e+00	2.42e+00	2.42e+00	2.42e+00	2.42e+00	1.84e+00	1.84e+00	1.84e+00	1.84e+00	1.40e+00	1.40e+00		1.40e+00	1.40e+00	1.40e+00

ALIGNMENTS

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Query Match Best Local Similarity Matches 154; Conse	HANDERSON TO STANK TO	; ;
ch 1 simi 154;	HMMAN S 95; Q93044; CV-1997 (REL CAUTION: REF FRAMESHIFTS: CAUTION: REF FRAMESHIFTS: FRAMESHIFTS	
98.9% larity 98.7%. Conservative	IEXI_HUMAN O1-NOV-1995 (REL. 32, CI) O1-NOV-1997 (REL. 35, LI) RODALING (HUMAN). EUKARYOTA; METAZOA; CHOI EUTHERIA; PETAMATES. [1] INDICENCE FROM N. A. MEDLING; 96181295 CANCER RES. 56:1498-150. [2] CANCER RES. 56:1498-150. [2] CANCER RES. 56:1498-150. [2] PRELLIMINARY SEQUENCE OF TISSUE-PLACENTA; HILLIER L., CLARK N., DI HULTMAN M., KUCABA T., RIFKIN L., ROHLETMO T., WILLIAMSON A., WOHLDMANI SUBMITIED (FEB-1995) TO O1-1 SUBCELLULAR LOCATION: BY RADIA; I-SUMILARITY: STRONG, I-CAUTION: REF. 2 SEQUI FRAMESHIFTS. EMBL; 749531; -, NOT_ANI GLYCOPROTEIN; TRANSMEMBI GLAMBLY 1933 133 CARBONYD 13 136 CARBONYD 13 136 CARBONYD 13 CARBONYD 13 136 CARBONYD 13 CARBONYD 13 CARBONYD 13 CARBONYD 14 CARBONYD 15 CARBONYD 15 CARBONYD 15 CARBONYD 15 CARBONYD 15 CARBONY	
98.9%; 98.7%; vative	IEXI_HUMAN STANDARD; PRT; 156 AA. P46695; Q93044; 01-NOV-1995 (REL. 35, LAST SEQUENCE UPDATE) 01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE) 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE) 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE) 101-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE) 101-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE) 101-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE) 102-INATION-INACIONAL CHORDATA; VERTEBRATA; TETRAPODA; 103-INACIONAL CHORDATA; 103-INACIONAL CHORDATA; 103-INACIONAL CHORDATA; 104-INACIONAL CHORDATA; 104-INACIONAL CHORDATA; 105-INACIONAL CHORDATA; 105-INACION	
Score Pred. 1; }	ARD; PRT; 156 AA. , CREATED) , LAST SEQUENCE UPDATE) , LAST ANNOTATION UPDATE) , LAST ANNOTATION UPDATE) , LAST ANNOTATION UPDATE) , LAST ANNOTATION UPDATE; IMMEDIATE-EARLY GENE IEX- CHORDATA; VERTEBRATA; TET 1502(1996). OF 1-106 FROM N.A. OF 1-106 FROM N.A. OF 1-106 FROM N.A. OF 1-1	
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MPsrch_nn n.a. - n.a. database search, using Smith-Waterman algorithm

Thu Apr 23 05:08:39 1998; MasPar time 999.58 Seconds 1452.649 Million cell updates/sec

Tabular output not generated.

Description: >US-08-799-910-9 (1-1228) from US08799910.seq 1228

Perfect Score: N.A. Sequence: Comp:

Scoring table: TABLE default Gap 6

Nmatch STD : Dbase 0; Query 0

354530 seqs, 591221332 bases x 2

Post-processing: Minimum Match 0% Listing first 45 summaries

1:em_in 2:em_or 3:em_om 4:em_ov 5:em_pl 6:em_htg
7:em_hum1 8:em_hum2 9:em_ba 10:em_ro 11:em_un 12:em_vi
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Database:

14:gb_ro 15:gb_om 16:gb_ov 17:gb_in 18:gb_pl 19:gb_ba 20:gb_st 21:gb_vi 22:gb_ph 23:gb_sy 24:gb_un 25:gb_pat 26:gb_htg

Statistics: Mean 11.417; Variance 7.667; scale 1.489

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Query Query Query Query Match Length DB ID Description 9.6 1938 14 MMGLY96 M.musculus gly96 mRNA. 9.3 1758 14 RNPRG1 R.norvegtcus PRG1 gene 6.4 7218 25 166494 Sequence 14 from paten 5.5 7218 25 166494 Sequence 14 from paten 3.0 215 25 128278 Sequence 5 from patent 3.0 10772 17 AF012089 Drosophila melanogaste 2.9 10772 17 AF012089 Drosophila melanogaste 2.1 215 25 128278 Sequence 5 from patent 3.0 10772 17 Sequence 5 from patent 3.1 25 25 128278 Sequence 5 from patent 3.2 24 800 16 GGU41467 Gallus gallus fibrobla 3.4 1125 15 SSL36LBP S.scrofa mRNA for L-36	11 29 12 29	10 29	c 7 35 8 33 9 29	c 5 41 6 37	2 114 3 79 C 4 67	No. Score	Result
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ALIGNMENTS

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Query Match Best Local Similarity 77.8%; I Matches 165; Conservative	/organisme mus musculus /strain="BALB/c" /db_xref="taxon:10090" 390 a 525 c 503 g 52	шн	glycosylated protein Oncogene 8 (3), 797-801 (1993) 93173526	(Losses 1 to 1935) Charles, C.H., Yoon, J.K., Simske, J.S. and Lau, L.F. Genomic structure, cDNA sequence, and expression of gly96, a growth factor-inducible immediate-early gene encoding a short-lived	Direct Submission Submitted (29-JUL-1992) L. Lau, University of Inhinois College of Med., Dept. of Genetics, M/C 669, 808 South Wood Street, Chicago, IL 60612, USA	<pre>Vertebrata; Eutheria; Rodentia; Sciurognathi; Myomorpha; Murinae; Mus. 1 (bases 1 to 1938) Lau, L.</pre>	9287803 gly96 gene; glycosylated protein. house mouse. Mus musculus Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;	MMGLY96 1938 bp M.musculus gly96 mRNA. X67644
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163; Conservative
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X96437
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Dorner,F., Scheiflinger,F. and Falkner,F.Gunter.
Recombinant fowlpox virus
Patent: US 5670367-A 14 23-SEP-1997;
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166494
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Dorner,F., Scheiflinger,F. and Falkner,F.
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128278
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Bennett,A., Labavitch,J.M., Powell,A. and Stotz,H.
Plant inhibitors of fungal polygalacturonases and their use
control fungal disease
Patent: US 5569830-A 5 29-OCT-1996;
 AF012089
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Pred. No. 5.19e-06;
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Gray,Y.H.M., Sved,J.A.,
Direct Submission
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1 (bases 4546 to 4553)
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Drosophila melanogaster
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6476. .6690
/gene="CP1"
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/gene="CP1"
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/gene="CP1"
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/gene="CP1"
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/gene="CP1"
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2427. .
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/db_xref="pi0:92305221"
/db_xref="pi0:92305221"
/translation="keravullpllallavaQavsfadvvmeewhjfklehrknyodet
EERFRLKIFNENKHKIAKHNQRFAEGKVSFKLAVNKYAQLLHHEFRQLMNGFNYTLHK
QLRAADESFKGVTFISPAHYTLPKSVDWRTKGAVTAVRQQGHOEKSYSYFKALEGQ
HFRKGGVLVSLISEQNLVDCSTRYGNUCCNGGLMDNAFRYIKDNGGFDYEKSYPVEALD
DSCHFNKGTVGATDRGFTDIPQGDEKKMAEAVATVGPVSVAIDASHESFQFYSEGVYN
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/gene="CP1"
join(<8110. .9300,9370. .>9532)
/product "phenylalany1 tRNA synthetase"
/join(8110. .9300,9370. .>9532)
/note="potential orf"
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/db_xref="taxon:7227"
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of Sydney, Biology Al2, Sydno
Location/Qualifiers
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Gray,Y.H.M., Sved,J.A.,
Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Drosophila melanogaster
Eukaryotae; mitochondrial eukaryotes; Metazoa; Arthropoda;
Tracheata; Hexapoda; Insecta; Pterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila
1 (bases 4546 to 4553)
Gray, Y. H., Tanaka, M. M. and Sved, J. A.
P-element-induced recombination in Drosophila melanogaster: h
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Drosophila melanogaster cysteine proteinase-1 (CP1) gene,
Cds, and phenylalanyl tRNA synthetase gene, partial cds.
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TDGWTNVTPKILSYVGANKHLQTDHPLSIIRQRIVNYFYGAYRNQRGNPLFSVYDQMN
PVVTVQQNFDNLLIPADHVSRQXSDCYYINQQHLLRAHTTAHQVELISGGLDMFLVVG
EVYRRDEIDSTHYPVFHQADAVRLVTKDKLFERNPGLEFETWSGTLADPKLILPHP
SSWTKPNSPATRRAVKLMEHEMKHVLVGLTKDLFGPRIKYRWDTYFPPTQPSWELEI
YFKDNWLEVLGCGIMRHEILQRSGVHQSIGYAFGVGLERLAMVLFDIPDIRLFWSNDS
GFLSQFSEKDLHNLPKYKPISHYPQCINDLSFWLPQDIEVDAGFSPNDFYDLVRSVAG
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/gene="CP1"
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/db_xref="PID:g2305222"
2310. .2426
/gene="CP1"
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∕gene≖"CP1"
                                                                                                                                                                                                                                                   /organism="Drosophila melanogaster"
/db_xref="taxon:7227"
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I28278
g1819054
 l (bases 1 to 215)

Bennett, A., Labavitch, J.M., Powell, A. and Stotz, H. Plant inhibitors of fungal polygalacturonases and control fungal disease Patent: US 556980-A 5 29-OCT-1996;
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Similarity 19.0%;
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SSWTKDNSPATRRAVKLMEHENKHVLVGLTKDLFGPRIXYRWVDTYFPFPGPSWELEI
YFKDNWLEVLCGGIMEHEILQRSGVHOSIGYARFGVGLERLAMVLFDIRDIRLTKYSNDS
GFLSQFSEKDLHNLPKYKPISHYPQCTNDLSFWLPQDIEVDAGFSPNDFYDLVRSVAG
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/db_xref="pid:92305222"
/db_xref="pid:92305222"
/translation="MLTLRYOGARHWIKSTRCLASSAAPAKSPSSPPQLEVSGSTYA
TDGWTNVTPKILSYVGANKHLQTDHPLSIIRQRIVNYFYGAYRNQRGNPLFSVYDQMN
PVVTYQQNFDNLLIPADHVSRQKSDCYYINQQHLLRAHTTAHQYELISGGLDNFLVYG
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/gene="CP1"
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EERFRLKIFNENKHKIAKHNQRFAEGKVSFKLAVNKYADLLHHEFRQLMNGFNYTLHK
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/product="cysteine proteinase-1"
/db_xref="pID:g2305221"
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                                                                  Local Similarity
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  ATGGGGAGGACTCGGGTGGGGAGGACGTCCCGGCTGGGATGAAGTCTGGTGGTGGGTCG
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Gallus gallus
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Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Archosauria; Aves; Neognathae; Galliformes;
Phasianidae; Phasianinae; Gallus.

1 (bases 1 0800)
                                                                                                                                                                                                                                                                                                                    Submitted (27-NOV-1995) Philip H. Crossley, Parnassus, San Francisco, CA 94143-045, USA Location/Qualifiers
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96140646
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                                                                                                                                                                                                                             /organism="Gallus gallus"
/db_xref="taxon:9031"
/dev_stage="embryo"
/tissue_type="brain"
/clone_lib="E10 embryonic c
<1. .615
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FGF8 mRNA, partial cds.
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Submitted (18-MAY-1994) E.J. O'Keefe, 1
137 NCMH, Dept of Dermatology, CB7600,
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S.scrofa mRNA for
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Vertebrata;
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                           1 (bases 1 to 1266)
Yang, Z. and Wensel, T.G.
Molecular cloning and functional expression
mammalian inorganic pyrophosphatase
J. Biol. Chem. 267, 24641-24647 (1992)
                                                                                                                                                                                                                                                                                                                                                     g163228
                                                                                                                                                                                                                                                                                                                                                                                Bovine inorganic
M95283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2.48;
Similarity 89.28;
33; Conservation
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                                                                                                                                                                                              Bukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Artiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                                                                                                                                                                                                                Bos taurus
                                                                                                                                                                                                                                                                                           inorganic pyrophosphatase
Bos taurus retina cDNA to
                                                                                                                                                                                                                                                                                                                                                                                                                                         BOVIOPPP
                                                                                                                                                                         Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Biol. Chem. 269 (50), 31770-31776 (1994)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KSLVINFKVGSSGDVALHINPRLTEGIVVRNSYLNGKWGAEERKSSFNPFAPGQYFDI
SIRCGLDRFKVYANGQHLFDFSHRLSNFQGVDTLEIQGDVTLSYVQI"
1 347 c 303 g 220 t
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/product="1-36 lactose binding protein"
/product="1-36 lactose binding protein"
/db_xref="piD:9623346"
/db_xref="piD:9623346"
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/translation="MAFVPAPGYOPTYNPTLPYYKPIPGGLRYGMSVYIOGVANEHMK
/translation="MAFVPAPGYOPTYNPTLPYYKPIPGGLYARRTIVIKGYYPPSGLYARKTIVIKGYYPPSGMPNPGYPGPGKHNQQPCNLPCMEGAPTFNPPVPYKTRLQGGLYARRTIVIKGYYPPSGMPNPGYPGPGFGKHNQQPCNLPCMEGAPTFNPPVPYKTRLQGGLYARRTIVIKGYYPPSGMPNPGYPGFGFGKHNQQPCNLPCMEGAPTFNPPVPYKTRLQGGLYARRTIVIKGYYPPSGMPNPGYPGFGFGKHNQQPCNLPCMEGAPTFNPPVPYKTRLQGGLYARRTIVIKGYYPPSGMPNPGYPGFGFGKHNQQPCNLPCMEGAPTFNPPVPYKTRLQGGLYARRTIVIKGYYPPSGMPNPGYPGFGFGKHNQQPCNLPCMEGAPTFNPVPYKTRLQGGLYARRTIVIKGYYPPSGMPNPGYPGFGFGFGFTNPVPYKTRLQGGLYARRTIVIKGYYPPSGMPNPGYPGFGFTNPVPYKTRLQGGLYARRTIVIKGYYPPSGMPNPGYPGFTNPVPYKTRLQGGLYARRTIVIKGYYPPSGMPNPGYPGFTNPVPYKTRLQGGLYARRTIVIKGYYPPSGMPNPGYPGFTNPVPTNPVPTNPTNPVPTNPTNPVPTNPVPTNPTNPVPTNPVPTNPVPTNPVPTNPVPTNPVPTNPVPTNPVPTNPVPTNPVPTNPVPTNPVPTNPVPTNPVPTNPVPTNPVPTNPVPTNPVPTNPVPTNPVPTNPVPTNPVPTNPVPTNPVPTNPVPTNPVPTNPVPTNPVPTNPVPTNPVPTNPVPTNPVPTNPVPTNPVPTNPVPTNPVPTNPVPTNPVPTNPVPTNPVPTNPVPTNPVPTNPVPTNPVPTNPVPTNPVPTNPVPTNPVPTNPVPTNPVPTNPVPTNPVPTNPVPTNPVPTNPVPTNPVPTNPVPTNPVPTNPVPTNPVPTNPVPTNPVPTNPVPTNPVPTNPVPTNPVPTNPVPTNPVPTNPVPTNPVPTNPVPTNPVPTNPVPTNPVPTNPVPTNPVPTNPVPTNPVPTNPVPTNPVPTNPVPTNPVPTNPVPTNPVPTNPVPTNPVPTNPVPTNPVPTNPVPTNPVPTNPVPTNPVPTNPVPTNPVPTNPVPTNPVPTNPVPTNPVPTNPVPTNPVPTNPVPTNPVPTNPVPTNPVPTNPVPTNPVPTNPVPTNPVPTNPVPTNPVPTNPVPTNPVPTNPVPTNPVPTNPVPTNPVPTNPVPTNPVPTNPVPTNPVPTNPVPTNPVPTNPVPTNPVPTNPVPTNPVPTNPVPTNPVPTNPVPTNPVPTNPVPTNPVPTNPVPTNPVPTNPVPTNPVPTNPVPTNPVPTNPVPTNPVPTNPVPTNPVPTNPVPTNPVPTNPVPTNPVPTNPVPTNPVPTNPVPTNPVPTNPVPTNPVPTNPVPTNPVPTNPVPTNPVPTNPVPTNPVPTNPVPTNPVPTNPVPTNPVPTNPVPTNPVPTNPVPTNPVPTNPVPTNPVPTNPVPTNPVPTNPVPTNPVPTNPVPTNPVPTNPVPTNPVPTNPVPTNPVPTNPVPTNPVPTNPVPTNPVPTNPVPTNPVPTNPVPTNPVPTNPVPTNPVPTNPVPTNPVPTNPVPTNPVPTNPVPTNPVPTNPVPTNPVPTNPVPTNPVPTNPVPTNPVPTNPVPTNPVPTNPVPTNPVPTNPVPTNPVPTNPVPTNPVPTNPVPTNPVPTNPVPTNPVPTNPVPTNPVPTNPVPTNPVPTNPVPTNPVPTNPVPTNPVPTNPVPTNPVPTNPVPTNPVPTNPVPTNPVPTNPVPTNPVPTNPVPTNPV
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/cell_type="keratinocyte"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'gene="1361bp"
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Eutheria; Artiodactyla; Suiformes;
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L-36 lactose binding
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Pred. No. 1.36e+00;
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Suina; Su
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heat shock protein 70; heat shock protein homologue.
heat shock protein 70; heat shock protein homologue.
Dirofilaria immitts adult cDNA to mRNA.
Dirofilaria immittis eukaryotes; Metazoa; Nematoda;
Eukaryotae; mitochondrial eukaryotes; Metazoa; Nematoda;
Secernentes; Spiruria; Spirurida; Spirurina; Filarioidea;
                                                                        Mus musculus
Y13071
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 (bases 1 to 1294)
Culpepper, J.A., Friedman, L. and Dale, B.
Molecular cloning and characterization of
cDNA encoding an Hsp 70 homologue
Mus musculus
                            complex.
                                         g2505939
26s proteasome;
                                                                                                 MM26SPROT
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              house mouse.
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                                                                                                                                                                                                                                                                                                                        /product="heat shock protein 70"
/db_xref="piD:g156706"
/translation="rfeelcadlfrsTmDpvekalrdakmDkAQVHDIVLVGGSTRIP
KVQKLLSDFFSGKELNKSINDDEAVAYGAAVQAAILSGDKSEAVQDLLLLDVAPLSLG
IETAGGVMTALIKRNTTIPTKYSQTFTTYSDNQPGVLIQVYEGERAMYKDNNLLGKFE
LSGIPPAPRGVPQIEVTFDIDANGILNVSAQDKSTGKQNKITIINDKGRLSKDEIERM
VQEAEKYKADDEAQKDRIAAKNALESYAFNMKQTIEDEKLKDKISEDDKKKIQEKCDE
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239 c 300 g
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                                                                                                                                                                                                                                                                                                                                                                                                                                          'note="homologue"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Dirofilaria immitis"
/db_xref="taxon:6287"
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/db_xref="taxon:9913"
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mRNA
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kDa heat
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1.36e+00;
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                                                                                                                                                                                                                                                                               African clawed frog.

Xenopus laevis

Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;

Vertebrata; Amphibla; Batrachia; Anura; Mesobatrachia; Pipoidea

Pipidae; Xenopodinae; Xenopus.

1 (bases 1 to 1811)

Cordes, V.C., Reidenbach,S., Rackwitz,H.R. and Franke,W.W.

Identification of protein p270/Tpr as a constitutive component

the nuclear pore complex-attached intranuclear filaments

J. Cell Biol. 136 (3), S15-529 (1997)

27177132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Xenopus laevis nuclear pore complex-associated mRNA, partial cds.

U69669
                                                                                                                                                     Direct Submission Submitted (06-SEP-1996) Cell Biology/0110,
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Developmental Genetics, Western
Edinburgh EH4 2XU, UK
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Penney,M., Wilkinson,C., Wallace,M., Javerzat,J.P., Seeger,M.,
Dubiel,W., Toda,T., McKay,S., Allshire,R. and Gordon,C.
Multidrug resistance is mediated by the 26S proteasome in fission
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Direct Submission
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Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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34; Conser
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/product="255 proteasome, non-atpase subunit"
/product="255 proteasome, non-atpase subunit"
/db_xref="piD:e352083"
/db_xre
/organism="Xenopus laevis"
/db_xref="taxon:8355"
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/db_xref="taxon:10090"
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Pred. No. 1.36e+00;
0; Mismatches 5;
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stern General Hospital, Crewe Roa
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TITLE
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Best Local Similarity
Matches 40; Conser
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Gene 200 (1-2), 1-10 (1997)
98038971
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West,M.C., Kozarov,E. and Teng-umnuay,P.
Direct Submission
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The cytosolic glycoprotein FP21 of Dictyostelium discoideum is encoded by two genes resulting in a polymorphism at a single amino
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larity 78.4%;
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GTDPDTETEDSKTAGEGKVQAADSQNIGDSGVVTAESTTSQETERQP SSASDRQGPRP
PQSPRRQAHPFRLTILAPPQELGPPPAQRIFVALRQSVGRGLQLLTPGVGGMQHFFDEE
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STGNVPTSVDSGAADEGDEVFVEAESEGIGAESTLEMDTQQEEPVQPSEADLPSTSQD
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SSSIPKRPREEEEDSTIETPEQIADDTDQQRTKKRKEEDIEEKTETEAVINTEDALHI
LTQCSNMEFPLEEEIVESPIQTSQVIESQAPEQLQNVQSTQDSLQDTPPKKTHNLVIV
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translocated promotor region"
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RNYLDIKPLLDVTCKTVANMIRGKTPBEIRKIFNIKNDFTPEEDEQIRKENEWCEDKG
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1158. .1311
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//gene="fpa2"
//oct--"-"
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/clone_lib="Uni-ZAPTMXR library, Stratagene"
                                                                                                                                                                                                                                           1061. .1703
/gene="fpa2"
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Matches
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                                       2.48;
Similarity 87.28;
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144	DNA sequence 4.	ric DNA sequence 1.	NN	probe 8.0	201	genome fragment 1.1 Natriuretic Pep 5.0	Pre	•	predicted by chance to have a score of the result being printed total score distribution.	.778; scale 1.381	part9 10:part10 11:part11 12:part12 13:part1 15:part15 16:part16 17:part17 18:part18 20:part20 21:part21 22:part22 23:part23 25:part25 26:part26 27:part27 28:part28 30:part30 31:part31 32:part32 33:part33	4:part4 5:part5 6:part6 7:part	ia	ės x 2			seq TGAaaaaaaaaaaacicgag ACTITTTTTTTTTTGAGCTC	899.629 Million cell updates/sec	MasPar time 157.52 S	using Smith-Waterman algorithm	Biocomputing Research Unit. sity of Edinburgh, U.K. Oxford Molecular Ltd	*****************			安全安全安全安全安全安全安全安全安全安全安全安全安全安全安全安全安全安全安全
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ALIGNMENTS

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ID 077534; standard; DNA; 297 BP.

AC 077534;

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DB 2; L 5.93e-35;

Length 1047;

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23-JUN-1989; US-370673.
(GETH ) GENENTECH INC.
Chang M, Goeddel D, Lowe D
WPI; 91-036711/05
                 Natriuretic protein receptor B - for diagnosis and treatment of kidney failure, heart failure, hyperaldosteronism, glaucoma etc. Claim 3; Fig 1; 49pp; English.

The sequence was derived from the DNA encoding natriuretic peptide receptor B, NPRB, having guanyl cyclase (GC) activity and protein kinase activity. The DNA can be inserted into expression vectors for the prodn. of the protein, opt. after being mutated to produce NPRB analogues. The protein has a mol wt. of 115 kD (calculated Mr-RPRB analogues. The protein (or variants) can be used in treatment of natriuretic peptide disorders, and also to isolate peptides using affinity chromatography. Antibodies with affinity for NPRB can
                                                                                                                                                               WPI; 91-036711/05.
N-PSDB; Q10324.
                                                                                                                                                                                                                                                                                                                                                                                                                               /note= "GC and protien kinase activity"
Modified -site 24..26
/label= N-glycos_site
Modified -site 35..37
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Human Natriuretic Peptide Receptor B.
HURB; ANP; BNP; CNP; kidney failure;
hyperaldosteronism; glaucoma; guanyl
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Q10572;
          also be prepd
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Modified -site 349..351
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/label= N-glycos_site
/label= N-glycos_site
/modified -site 277. 279
                                                                                                                                                                                                                                                                                                                                                                              /label= N-glycos_site
Modified -site 195..197
                                                                                                                                                                                                                                                                                                                                                                                                      /label= N-glycos_site
Modified -site 161..163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /label= extracellular domain /note= "binds natriuretic peptides
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d -site 600..602
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Best Local Similarity 9.0%.
Matches 83; Conservative
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                                                                                          nanandsvtnynsdnvgntansanstnmnvvtnnndnytcndanndnndvykvntngday
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RESULT ID Q1 AC Q1 DT 09

Q10572 standard; DNA; 1047 Q10572; 09-APR-1991 (first entry)

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Best Local S
Matches
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23-JUN-1989; US-370673.
(GETH) GENENTECH INC.
Chang M, Goeddel D, Lowe D
WPI; 91-036711/05.
                                                                                                                                                                                                                                                      Natriuretic protein receptor B - for diagnosis and treatment of kidney failure, heart failure, hyperaldosteronism, glaucoma etc. Claim 3; Fig 1; 49pp; English.

The sequence was derived from the DNA encoding natriuretic peptide receptor B, NPRB, having guanyl cyclase (GC) activity and protein kinase activity. The DNA can be inserted into expression vectors for the produc of the protein, opt. after being mutated to produce NPRB analogues. The protein has a mol wt. of 115 kD (calculated Mr=114,952). The protein has a mol wt. of 15 kD (calculated Mr=14,952) affinity chromatography. Antibodies with affinity for NPRB can also he prepare
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/note- "GC and protien kinase
Modified site 24.26
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Modified -site 244..246
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Modified -site 195..197
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Modified -site 35..37
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/note= "binds natriuretic peptides
Domain 456.456
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Modified -site 161. 163
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                                                            kngnnvvtnhghnnwtaraannyndartddrnhyntnngvnnanngsnnsvnhnvyarnn
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d -site 600..602
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d -site 349..351
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larity 8.5%;
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Pred. No. 2.20e-
248; Mismatches
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13-JUL-1993; G01467.
13-JUL-1992; GB-014857.
13-JUL-1992; GB-014857.
(MEDI-) MEDICAL RES COUNCIL.
GROSS J. Hadfield KM, Howel
Sibson DR, Starkey M;
WPI: 94-035056/04
           New nucleic acid fragment encoding gene products - can be used for genetic analysis and mapping claim 1; Page 586; 616py. English.

Human nucleic acid fragments, isolated from brain, adrenal tissue the placenta or bone marrow comprise any of: (A) a sequence as elected from (Q/6401-Q/7613), (B) an allelic variation of a sequence as described in (A), or (C) a sequence complementary to (A) or (B).

Preferred sequences exhibit no more than 90105mology to a human
                                                                                                                                                                                                                                                                                                 23-SEP-1994 (first entry)
Human genome fragment. (Preferred)
Brain; placenta; bone marrow; genetic analysis; gene mapping;
detection; homology; human; adrenal tissue; ds.
                                                                                                                                                                                                                                                                                                                                                                   Q77554 standard;
Q77554;
sequence
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WO9401548-A.
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                                                                                                                                                                                                                               CC double-stranded DNA (or its complementary strand or the corresp. CC double-stranded DNA) which comprises one of the 7837 "GS" sequences given in T19001-T26837 and which is able to hybridise to part of CC human genomic DNA, cDNA or mRNA is claimed. The GS (Gene Signature) Sequences were obtained from 3'-directed cDNA libraries prepared from various human tissues; synthesis of cDNA was initiated from the 3'-cuntranslated sequence is unique to a particular mRNA species, almost all the 3'-oriented cDNAs hybridise with specific mRNAs. Each library is constructed so as to reflect accurately the relative abundance of different mRNAs in the particular tissue from which it was derived. The appearance frequency of a given GS in a cDNA library can be constructed as a means of diagnosing abnormal cell function or for recognising different cell types.

So Sequence 53 BP; 18 A; 9 C; 9 G; 17 T;
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Best Local S
Matches 4
OS1746 standard; cDNA; 91 BP.
OS1746; Standard; cDNA; 91 BP.
OS1746;
31 MAY-1994 (first entry)
Oligonucleotide probe MK14-A
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                                                                                                                   Gene signature; messenger RNA; mRNA; relative abundance; frequency human; cloning; mapping; non-biased library; diagnosis; detection; cell typing; abnormal cell function; ss.
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A single-stranded DNA (or its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matsubara K, Okuk
WPI; 95-206931/27.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gene signature;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Identifying gene signatures in 3'-directed human cDNA library -
for diagnosis of abnormal cell function, by preparing cDNA that
reflects relative abundance of corresp. mRNA in specific human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11-NOV-1994; J01916.
12-NOV-1993; JP-355504
(MATS/) MATSUBARA K.
(OKUB/) OKUBO K.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               standard;
                                                                                                                                                                            h 3.8%;
Similarity 100.0%;
47; Conservative
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llarity 75.0%;
Conservative
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          mycobacteria;
                                                                                                                                                                          Score 47; DB 18
Pred. No. 2.61e:
0; Mismatches
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Pred.
0; M
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d. No. 6.80e-18;
Mismatches 35
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2.61e-10;
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          disease
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Best Local Similarity
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Best Local
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Claim 3; Page 14; 23pp; English.
Claim 3; Page 14; 23pp; English.
Oligonucleotide probe MK14-A consists of nucleotides
(051735). It hybridized to all spp. of mycobacteria tested,
cross reacted to a few non-mycobacterial spp. The probe may
be useful as an initial screen for mycobacterial infection.
See also Q51735-45 and Q51747-59.
See also Q51735-45 and Q51747-59.
Tength 91;
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Synthetic.
EP-571911-A.
01-DEC-1993; 108325.
24-MAY-1992; US-889651.
26-MAY-1992; US-889651.
(BECT ) BECTON DICKINSON C
Shank DD, Spears PA;
WPI; 93-378844/48.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Synthetic.
EP-571911-A.
01-DEC-1993.
24-MAY-1993; 108325.
26-MAY-1992; US-889651.
                                                                                                                                                                                                                                                                            1153
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 3; Page 14; 23pp; English.
Oligonucleotide probe MK14-A consists of nucleotides 5-85 of (051735). It hybridized to all spp. of mycobacteria tested, cross reacted to a few non-mycobacterial spp. The probe may be useful as an initial screen for mycobacterial infection. See also Q51735-45 and Q51747-59.
Sequence 91 BP; 5 A; 17 C; 15 G; 4 T;
                                            N81164 standard; DNA; 204 BP.
N81164;
08-NOV-1990 (first entry)
Base substituted E.coli beta-galactosidase alpha-fragment.
E.coli beta galactosidase alpha-fragment; base substitutic
Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (BECT ) BECTON DICKINSON Shank DD, Spears PA; WPI; 93-378844/48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      samples
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Q51746;
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larity 2.0%;
Conservative
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larity 13.3%;
Conservative
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Pred.
45; M
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Pred. No. 8.07e-10;
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No. 2.31e-08
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Best Local S
Matches 1
                                                                                            05-MAY-1988.
30-WAR-1988; 105163.
03-APR-1987; US-034819.
(SUSO) SUOMEN SOKERI OY.
Lehtovaara P, Knowles J, MPI; 88-279927/40.
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Random point mutations were introduced into the alpha fragment of E.coli beta-galactosidase. The wild type sequence was obtained as a single stranded template and an oligonucleotide was hybridised to it to generate a popn of DNA molecules which terminate at all possible nucleotide positions within a specified region. The variable 3' ends generated in this way are used as primers for reverse transcriptase. Nucleotides are misinocorporated by the transcriptase and the molecules are completed to forms that can be amplified and then expressed in a suitable host-vector system. The sequence covers all 176 difft base substitutions, most of which
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03-APR-1987; US-034819.
(SUSO) SUOMEN SOKERI OY
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           Introducing random point mutations into nucleic acods by prepn of single stranded template, annealing a primer, elong misincorporation, completion of molecules and screening. Disclosure; p; English.

Random point mutations were introduced into the alpha fragment E.coli beta-galactosidase. The wild type sequence was obtained
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Base substituted E.coli beta-galactosidase alpha-fragment.
E.coli beta galactosidase alpha-fragment; base substitutions;
Escherichia coli.
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N81164;
                                                                                                                                                                              EP-285123-A.
                                                                                                                                                                                                     primer_bind
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primer_bind 187..204
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18; Conser
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Pred. No.
61; Misma
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PT Identifying proteins or peptide(s) which bind a ligand - by screening a recombinant vector library expressing fusion proteins processing a binding domain and an effector domain proteins promprising a binding domain and an effector domain proteins promptising a binding domain and an effector domain proteins of prot
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01-FEB-1993;
30-DEC-1993;
31-JAN-1994;
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Fowlkes DM, Kay BK;
WPI; 94-279739/34
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29; Conser
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; US-176500.
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Pred. No. 2.
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PT Identifying proteins or peptide(s) which bind a ligand - by Identifying proteins or peptide(s) which bind a ligand - by screening a recombinant vector library expressing fusion proteins processing a binding domain and an effector domain

Screening a personal protein of the peptides. This generic formula can also be converted as follows: x(NNB)1(CAC)(NNB)1(CAC)(NNB)1(CAC)(NNB)1(CAC)(NNB)1(CAC)(NNB)1(CAC)(NNB)1(CAC)(NNB)2z(NNB)6.

CC (Also not the same as y) that are not specified further. The peptides comparated by this and other generic sequences (70470-73) have invariant the protein of the same as y) that are not specified further. The peptides concatenated by this and other generic sequences. Takes are concatenated by this and other generic sequences. Takes are concatenated heterofunctional proteins or peptides, comprising at least two functional regions - a binding domain with affinity for a ligand and a second effector peptide portion that is chemically or biologically can be used in the two functional regions. Comprise a linker peptide between the 2 domains. The TSARs or compans. comprise a linker peptide between the 2 domains. Compans to the cell. They can also replace the function of macromolecules, eg. mental concepts and the cell. They can also replace the function of macromolecules, eg. mental concepts whether the production. The TSARs are easily characterised and have designed activity allowing direct and rapid detection in a screening process.

CC monoclonal or polyclonal antibodies and therefore circumvent the need for complex methods of hybridoma formation or in two antibody.

CC manner the can also replace the function of macromolecules, eg. metal concepts and the concepts and have designed activity allowing direct and rapid detection in a screening process.
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01-FEB-1994;
01-FEB-1993;
01-DEC-1993;
31-JAN-1994;
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Fowlkes DM, Kay BI
WPI; 94-279739/34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Generic DNA sequence to generate a random TSAR peptide library. TSAR; totally synthetic affinity reagent; synthetic; binding dor effector domain; concatenated heterofunctional protein; linker; direct; rapid; detection; screening; treatment; generic; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 P-PSDB;
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2.9%;
Local Similarity 10.1%;
nes 11; Conservativo
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114 BP; 0 A; 4 C
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NORTH CAR
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32; |
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                       DB 12;
1.32e-04;
                                                                               G;
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0 T;
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RESULT
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                                                                                                                                                                                                                    CC Q70468 is a generic DNA sequence used to generate random TSAR (Totally CC Q70468 is a generic DNA sequence) used to generic formula can also be compresented as follows: X(NNB)11(TGC)(NNB)6Z(NNB)7(TGC)(NNB)10X. X CC and x are flanking restriction sites (X is not the same as y) that are cont specified further. Other generic sequences are shown in Q70466-68. CC chemically or peptides generated by these generic sequences are shown in Q70466-68. CC comprising at least two functional regions - a binding domain with CC affinity for a ligand and a second effector peptide portion that is CC chemically or biologically active. They may further comprise a linker CC chicken the expressed peptide contains 2 or 4 cysteine residues positioned CC in, or flanking, the unpredicted or variant residues. These residues confer some degree of conformational rigidity to the peptides. The TSARS CC comprising a TSAR binding domain can be used in vivo to CC deliver a chemically or biologically active moiety, eg. metal ion, CC cradioisotope, peptide, toxin or enzyme, to the specific target or on the componex methods of hybridoma formation or in vivo antibody
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                δÃ
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01-FEB-1993; US-013416.

30-DEC-1993; US-176500.

31-JAN-1994; US-189331.

(UYNC-) UNIV NORTH CAROLINA.

FOwlkes DM, Kay BK;

WPI; 94-27979/34.
                                                                                                             for complex methods of hybridoma formation or in vivo antibody production. The TSARs are easily characterised and have designed activity allowing direct and rapid detection in a screening process. Sequence 114 BP; 0 A; 2 C; 2 G; 2 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Identifying proteins or peptide(s) which bind a ligand screening a recombinant vector library expressing fusion comprising a binding domain and an effector domain bisclosure; Page 35; 255pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        P-PSDB; R65154
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5, 9 or 12 nucleotides (see
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                          2.9%;
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Score
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34; M
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                                                        DB 12;
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                                                                                                                                                                                                                                                                                                                                                                                              PT comprising a focular vector and a effector domain

PS Disclosure; Page 35; 255pp; English.

CC Q70467 is a generic DNA sequence used to generate random TSAR (Totally

CC Synthetic Affinity Reagents) peptides. This generic formula can also be

CC represented as follows: X(NNB)16(TGC)(NNB)12(NNB)16(TGC)(NNB)1y. X

CC and Y are flanking restriction sites (X is not the same as Y) that are

CC not specific peptides generated by these generic sequences are shown in Q70466-68.

CC Other specific peptides generated by these generic sequences are shown in

CC R65131-54. TSARs are concatenated heterofunctional proteins or peptides,

CC comprising at least two functional regions - a binding domain with

CC affinity for a ligand and a second effector peptide portion that is

CC comprising at least two functional regions - a binding domain with

CC that the expressed peptide contains 2 or 4 cysteine residues positioned

CC in or flanking, the unpredicted or variant residues. These residues

CC composes comprising a TSAR binding domain can be used in vivo to

CC deliver a chemically or biologically active moiety, eg. metal ion,

CC composes, peptide, toxin or enzyme, to the specific target or on the

CC compose peptide toxin or enzyme, to the specific target or on the

CC compose of the periods of the function of macromolecules, eg.
                                                                                                                                                                                                                                                                               Query Match
Best Local
                                                                                                                                                                                                                                                                  Matches
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01-FEB-1994;
01-FEB-1993;
30-DEC-1993;
31-JAN-1994;
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Q70467 standard;
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                                                                                                                                                                                                                                                                                                                                complex methods of hybridoma formation or in vivo antibody production. The TSARs are easily characterised and have designed activity allowing direct and rapid detection in a screening process. Sequence 114 BP; 0 A; 2 C; 2 G; 2 T;
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Synthetic.
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                                Q70466 standard; DNA; 114 BP
Q70466;
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Generic DNA sequence to generate a random TSAR-9 petide library.
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                                                                                                                                                                                                                            TTCCCACCGGGCCTAGCCCCAGCTGGGCTGTGCCTCTGTCTATGCGCCTCGGTCTCTG 637
                                                                                                                         TGCGCCTCGGTCCCGCCTCAAGCACCGGGTGGCGTCTCCGCTGTAGTG
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                  (first entry)
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6, 9 or 12 nucleotides (see
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Pred.
33; M
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hes 71;
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Synthetic. WO9640162-A1.

chronic obstructive

pulmonary

disease; bronchitis;

cystic fibrosis;

Asthma;

19-DEC-1996; 06-JUN-1996;

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RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PT Identifying proteins or peptide(s) which bind a ligand - by screening a recombinant vector library expressing fusion proteins promprising a binding domain and an effector domain proteins promprising a binding domain and an effector domain proteins prot
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
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Best Local
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01 FEB-1994; U00977.

01 FEB-1993; US-013416.

30-DEC-1993; US-176500.

31-JAN-1994; US-189331.

(UUNC-) UNIV NORTH CAROLINA.
FOWLKES DM, KAY BK;
WPI, 94-279739/34.
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                                                                                                                                                 Human endothelin-1
                                                                                                                                                                                           T76405
                                                                                                                                                                                                               T76405 standard;
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                                                                                                                         ndothelin-1 antisense oligonucleotide. airway epithelium; adenosine free; cy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
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                                                                                                                                                                       (first entry)
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                                                                                                                                                                                                                 DNA;
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Pred. No. 4.59er05;
31; Mismatches 71
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ein; linker;
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Search completed: Thu Apr 23 05:42:23 1998 Job time: 162 secs.
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Chaim 6; Page 4; Page 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 2.9%;
Best Local Similarity 28.2%;
Matches 20; Conservative
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Metzger WJ, Nyce JW;
WPI; 97-051871/05.

Treatment of airway diseases such as asthma - by topically applying adenosine-free antisense oligo:nucleotide to airway epithelium of
                                                                                                                                                                                                                                                                                                subject
                                                                                                                                                  :::::|| ||
630 TCGGTCCCGCC 620
                                                                                                                                                                                                                                 165 cbbbbbcctcc 175
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Pred. No. 1.32e-04;
33; Mismatches 18; Indels
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Release 3.0.4A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1997 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

MPsrch_pp protein - protein database search, using Smith-Waterman algorithm Fri Apr 17 13:41:02 1998;

Tabular output not generated Run on: MasPar time 6.99 Seconds 310.069 Million cell updates/sec

Title: >US-08-799-910-10

Description: Perfect Scor Score: (1-156) from US08799910.pep

Sequence: 1 MCHSRSCHPTMTILQAPTPA.....EPSDYALDLSTFLQQHPAAF 156

Scoring table: PAM 150 Gap 11

111726 seqs, 13889129 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

a-geneseq30
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18
19:part19 20:part20 21:part21 22:part22 23:part23

Statistics: Mean 31.062; Variance 153.160; scale 0.203

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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Result No.	Score	Query Match	Length	BB	ID	Description	Pred. No.
1	101	9.1	183	23	W14570	Streptococcus pneumon	8.30e+00
2	100	9.0	439		R28150	Sugar beet chitinase	9.67e+00
w	98		520	9	R53072	Alpha 1b adrenergic r	1.31e+01
4	98		520		R52831	Sequence of human alp	1.31e+01
ر.	98	•	520		R85943	adr	1.31e+01
6	97	8.7	190	23	W14569	O	1.53e+01
7	97	8.7	1337	14	R85203	huDEP-1.	1.53e+01
œ	96		775		R66057	Human NMDAR2 receptor	1.78e+01
9	96		1214	12	R66065	Human NMDAR2 receptor	1.78e+01
10	96		1219	12	R66063	Human NMDAR2 receptor	1.78e+01
11	96		1231	12	R66062	Human NMDAR2 receptor	1.78e+01
12	96		1236	12	R66037	Human N-methyl-D-aspa	1.78e+01
13	96		1239	12	R66064	Human NMDAR2 receptor	1.78e+01
14	96	8.6	1244	12	R66061	Human NMDAR2 receptor	1.78e+01
15	95		198	10	R59841	ApoE4L protease.	2.06e+01
16	95		198	15	R92113	Human ApoE4L.	2.06e+01
17	95		311	10	R59843	ApoE4Lx2 protease.	2.06e+01
18	95		311	15	R92115	Human ApoE4Lx2.	2.06e+01
19	94		167	23	W14575	Streptococcus pneumon	2.40e+01
20	94	8.4	206	23	W14574	Streptococcus pneumon	2.40e+01

ğ Db

Query Match 9.1%; Best Local Similarity 26.7%; Matches 20; Conservative

Score 101; DB 23; Pred. No. 8.30e+00; 19; Mismatches 36

Length 183; Indels

0

Gaps

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4.	44	43	42	41	40	39	38	37	36	<u>ა</u>	34	ω ω	32	31	30	29	28	27	26	25	24	23	22	21
87	87	87	87	87	87	89	89	89	89	90	90	90	90	90	90	91	91	91	92	92	92	92	93	92
7.8	7.8	7.8	7.8	7.8	7.8	8 .0	8.0	8.0	8.0	8.1	8.1	8.1	8.1	8.1	8.1	8.2	8.2	8.2	ω	დ	ω ω	ω ω	ω	8
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<u>ا</u> ب	16	13	17	17	17	21	σ	σ	7	16	9	9	22	13	13	œ	11	23	18	9	4	N	ω	23
R05898	R94427	R79480	R96991	R94965	W00498	W14013	R30477	R32131	R40801	R89436	R56664	R51116	W18201	R78734	R78729	R52633	R60799	W14573	R91813	R51264	R77548	R10531	P60623	W14568
prod	ğ	Rat type II collagen.	Survival motor neuron	Survival motor neuron	Papillomavirus E2 bin			CMV Colburn region po	Beta.	α	Mutant platelet glyco	Platelet glycoprotein	Platelet glycoprotein	Human bone morphogene	Human bone morphogene	Guinea pig PH-30, 30	Rape abscission/dehis	Streptococcus pneumon	Hepatitis E virus str	HEV strain protein en	MEKK5 protein.	Prod. of DNA of pMG07		Streptococcus pneumon
٠	6.76e+0	6.76e+0		6.76e+0	٠.	5.04e+0	5.04e+0	5.04e+0	•			4.35e+0	4.35e+0	4.35e+0	4.35e+01	3.75e+0	3.75e+0	3.75e+0	3.23e+0	3.23e+0	3.23e+0	3.23e+01	2.79e+0	3.23e+0:

ALIGNMENTS

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Example 6; Fig 13; 296pp; English.

CC This sequence shows the central portion, including the C-terminus CC of the alpha-helix region and some of the proline-rich region, of CC pneumococcal surface protein A (PspA) of Streptococcus pneumoniae CC strain Bg9739. Comparison of the N-terminal and central regions CC (W14533-57 and W14562-91) of PspA polypeptides from different CC pneumococcal strains can be used to divide the strains into several CC framilles based on sequence homologies. PspA polypeptides, or CC fragments of them, can be used in vaccines to protect animals CC against S. pneumoniae infection and hence for the prevention of CC diseases such as otitis media, meningitis, bacteraemia and pneumonia. CC The sequence of the 3' half of the PspA alpha-helical region and the cc immediate 5' tip of the coding sequence are likely to be the critical sequences for predicting PspA cross-reactions and vaccine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT
                                                                                                                                                                                                                                                                                                                                                                                   16-SEP-1996; U14819.
15-SEP-1995; US-529005.
(UABR:) UAB RES FOUND.
Briles DE, Brooks-Walter A, C:
McDaniel LS, Swiatlo E, Tart R
WPI; 97-202002/18.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Streptococcus pneumoniae PspA central region. PspA; pneumococcal surface protein; vaccine; otitis media; meningitis; bacteraemia; pneumonia. Streptococcus pneumoniae strain Bg9739.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             JT 1
W14570 standard; Protein; 183 AA.
                                                                                                                                                                                                                                                                                                                                           Streptococcus pneumoniae surface protein PspC and truncated PspA -used in vaccines for protecting animals against S.pneumoniae % \left( 1\right) =\left\{ 1\right\} 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Streptococcus pneumoniae WO9709994-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         W14570;
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  28-OCT-1997
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183 AA;
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R, Yother
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RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
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Best Local :
21-SEP-1994 (first entry)
21-SEP-1994 (first entry)
Alpha lb adrenergic receptor.
Alpha lb adrenergic receptor.
PCR; amplification; prostatic hypertrophy; coronary heart disease; insulin resistance; hypertension; urinary retension; glaucoma; insulin resistance; hypertension; urinary retension; glaucoma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sugar beet chitinase 4 and corresponding DNA - inhibits germination and growth of chitin-containing fungi and is used to produce genetically transformed plants
Claim 5; Page 164-108; 254pp; English.
A clone encoding the chitinase 1 gene was isolated from a sugar beet EMBL3 genomic library. The sequence encodes a protein having 439 amino acid residues. Transgenic plants having increased resistance to nematodes and chitin-containing plant pathogens, partic. fungi, can be produced using genetic constructs containing the chitinase 1 gene. The protein itself can be used in fungicidal
                                                                                                                                                                       R53072 standard;
R53072;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            compositions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (DANI-) DANISCO AS.
Berglund L. Bojsen K, Mikkelsen JD,
WPI: 92-366261/44.
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08-APR-1991;
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/note= "possibly involved in anchoring
chitnase I protein to the cell wall
after modification of the prolines to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Region
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R28150 standard;
                                                                                                                                                                                                                                                                                                                                                    109
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Region 417..439
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d7..1'
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Similarity 30.1%;
25; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
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No. 9.67e+00;
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Alpha 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example; Page 46-51; 69pp; English.
The inventors claim a method of treating benign prostatic hyperplasia which comprises administering a therapeutically effective amount of a compound which binds to a human alphanetic and the second compound which binds to a human alphanetic accordance to the second compound which binds to a human alphanetic compound which binds to be a human alphanetic compound which be a human alphanetic compound whic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Treating benign prostatic hyperplasia - selectively to alphalC adrenergic recept of prostatic tissue
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Claim 43; Fig 2; 155pp; English.

In order to isolate a full length clone for the alpha 1 adrenergic receptor human cDNA libraries were screened by PCR with primers designed off the isolated genomic clones, from non conserved portions of the receptor gene. The PCR prod. was then used as a probe to isolate the full length alpha 1 adrenergic receptor gene. The gene can be used for screening for abnormalities associated with human alpha 1 adrenergic receptors, e.g. prostatic hypertrophy, coronary heart disease, insulin resistance, hypertension, urinary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14-APR-1994.
24-SEP-1993;
25-SEP-1992;
                       PCEXV-3-derived eukaryotic expression vector,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N-PSDB; Q62817
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See also R53071-3.
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NSDB, Q63181.
Alphal adrenergic receptor DNA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (SYNA-) SYNAPTIC PHARM CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12-NOV-1993; U10950.
13-NOV-1992; US-975867
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Bard JA, Forray C, Weinshe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12 TILQAPTPAPSTIPGPRRGSGPEIFTFDPLPEPAAAPAGRPSASRG
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41.38;
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ptor; antagonist; neuro
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Pred. No. 1.31e+01
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PT nucleic acids encoding related receptor subunits.

PT nucleic acids encoding related (079372) and subunit acceptor of all a.

PT nucleic acids encoding related (079372) with the exception of all a.

PT nucleic acids encoding related (079372) with the exception of all a.

PT nucleic acids encoding related (079372) with the exception of all a.

PT nucleic acids encoding related (079372) with the exceptor acide of the NMDAR2 (079378).

PT nucleic acids encoding related (079402). The clones are thought to be splice variants of each other. Based on the sequence of the 4 clones, a series of variants (079403-7) of the NMDAR2 receptor were constructed.

PT nucleic acids encoding the penes allows the reconstruction of the NMDAR compounds which be human numbar receptor.
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20-APR-1993; US-052449.
(SALK ) SALK INST BIOTECHNOLOGY IND ASSOC.
Daggett LP, Ellis SB, Liaw CW, Lu C;
WPI; 94-341863/42.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     06-JUL-1995 (first entry)
Human NMDAR2 receptor subunit clone NMDA21 protein.
N-methyl-D-aspartate; receptor; human; NMDA; cation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Key
Misc_difference 473..474
/note= "deletion of 17 a.a. from NM sequence between these residues"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-PSDB; Q79399.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human NMDAR2 receptor subunit clone NMDAR2C-delta15-delta51 gene N-methyl-D-aspartate; receptor; human; NMDA; cation-selective; clglutamate; hippocampus; rat; pcDNA1; NMDA receptor; antagonist.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 bind or are antagonistic to the human NMDA receptor. Sequence 775 \text{ AA};
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
20-APR-1994; U04387.
20-APR-1993; US-052449.
20-ALK | SALK INST BIOTECHNOLOGY IND ASSOC.
Daggett LP Ellis SB, Liaw CW, Lu C;
WPI; 94-341863/42.
N-PSDB; Q79407.
                                                                                                                                                                                                                                         Misc_difference 716..717
/note= "17 a.a. deletion
between these residues"
                                                                                                                                                                                                                                                                                                                                      Misc_difference 591..592
/note= "5 a.a. deletion of NMDAR2C a.a. sequence
between these residues"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         06-JUL-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R66065 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R66065;
                                                                                                                                                                                                                     WO9424284-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     iomo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     664 apppspcptprsgpspc1ptpdpppepsptgwgppdggra 703
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TPAPSTIPGPRRGSGPEIFTFDPLPEPAAAPAGRPSASRG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          h 8.6%;
Similarity 42.5%;
17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Protein; 1214
                                                                                                                                                                                                                                                                                   of.
                                                                                                                                                                                                                                                                                   NMDAR2C
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Pred.
11; M
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                                                                                                                                                                                                                                                                               a.a. sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 12; I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cation-selective; channel;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      channel;
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PS Claim 11: Page 99-104: 156pp: English.

PS Claim 12: Page 99-104: 156pp: English.

PS Claim 13: Page 99-104: 156pp: English.

PS Claim 14: Page 99-104: 156pp: English.

PS CL (NMDAP2C) gene clone NMDAR2C relata15-delta51. This clone covers the same sequence as the NMDAR2C relata15-delta51. This clone covers the Same sequence as the NMDAR2C receptor were constructed, by recombination, CC (079403-7) of the NMDAR2C receptor were constructed, by recombination, Dassed on the sequence of the 4 basic clones: NMDA21 (079399), NMDA22 (079401) and NMDA26 (079402). The NMDA receptor CC (079400), NMDA26 (079401) and NMDA26 (079402). The NMDA receptor CC (079400), NMDA26 (079375), DB (079377), DC and DD (079378). The receptor CC forms part of a family of NMDA receptors which have cation selective channels and bind glutamate and NMDA. The expression of the genes allows the reconstruction of the NMDA receptor. The complete receptor can be used to identify compounds which bind or are antagonistic to the human CC NMDA receptor.
                                                                                                                                                                                                                                  PT Isolated DNA encoding a human N-methyl-D-aspartate receptor
PT subunit - used as probes in the identification and isolation of
PT nucleic acids encoding related receptor subunits.
PT nucleic acids encoding related receptor subunits.
PS Claim II; Page 99-104; 156pp; English.

CC receptor receptor sequence of the novel N-methyl-D-aspartate (NMDA) receptor
CC c(NMDAR2C) gene clone pCMV-26-Scal-21-NocLI-24. This clone covers the
CC c(NMDAR2C) gene clone pCMV-26-Scal-21-NocLI-24. This clone covers the
CC come sequence as the NMDAR2C sequence but contains a deletion of a.a.
CC come sequence as the NMDAR2C sequence but contains a deletion of a.a.
CC contains the NMDAR2C protein (R66035). A series of variants (079403-7)
CC of the NMDAR2C protein (R66035). A series of variants (079403-7)
CC of the NMDAR2C receptor were constructed, by recombination, based on the
CC company of the Abasic clones: NMDAR21 (07939), NMDAR22 (079400), NMDAR24
CC sequence of the 4 basic clones: NMDAR21 (07939), NMDAR22 (079400), NMDAR24
CC sequence of the 4 basic clones: NMDAR21 (07939), NMDAR22 (079400), NMDAR24
CC sequence of the 4 basic clones: NMDAR21 (07939), NMDAR22 (079400), NMDAR24
CC sequence of the 4 basic clones: NMDAR2 receptor contains two subunits:
CC subunit R1 (079370) and subunit R2 selected from the subunits R2
CC (079375), 2B (079377), 2C and 2D (079378). The receptor forms part of a
CC (079375), 2B (079370), and subunit R2 selective channels and bind
CC family of NNDA receptors which have cation-selective channels and bind
CC reconstruction of the NNDA receptor. The complete receptor can be used to
Query Match
Best Local S
Matches
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human NMDAR2 receptor subunit clone pCMV-26-ScaI-21-NotI-24 protein. N-methyl-D-aspartate; receptor; human; NMDA; cation-selective; channel; glutamate; hippocampus; rat; pcDNA1; NMDA receptor; antagonist.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R66063 standard; Protein; 1219
R66063;
06-JUL-1995 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   27-OCT-1994.
20-ADR-1994; U04387.
20-ADR-1993; US-052449.
20-APR-1993; US-052449.
20-ADR-1993; US-052449.
20-ADR-1994; US-05249.
2
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/note= "17 a.a. deletion
between these residues"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NMDA receptor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO9424284-A.
                                                                                                                                                                                                               dentify compounds which bind
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18 TPAPSTIPGPRRGSGPEIFTFDPLPEPAAAPAGRPSASRG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                apppspcptprsgpspclptpdpppepsptgwgppdggra 946
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17; Conserv
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                                                                                                                                             1219 AA;
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llarity 42.5%;
Conservative
   8.6%;
llarity 42.5%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
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Pred. No.
11; Misma
   Score Pred. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NMDAR2C
                                                                                                                                                                                                               or are antagonistic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A
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                                     96; DB 12;
No. 1.78e+01
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. 1.78e+01
                                                                                                                                                                                                                   The complete receptor can be used antagonistic to the human NMDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12;
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                                                                      Length 1219;
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Similarity 17; Conser

Mismatches

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Gaps

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         PARTON PROPERTY OF THE PROPERT
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
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                                                                                                                                                                                                                                                                                                                                            Misc_difference 95
/note= "unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Streptococcus pneumoniae PspA central region.
PspA; pneumococcal surface protein; vaccine; otitis media;
meningitis; bacteraemia; pneumonia.
Streptococcus pneumoniae strain Bg8743.
Streptococcus pneumoniae strain Bg8743.
Streptococcus pneumoniae strain Bg8743.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     W14569 standard; Protein; W14569;
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Human alpha-1B adrenergic receptor DNA (see T03128) was cloned into the EcoI site of eukaryotic expression vector pCEXV-3. The resulting plasmid was co-transfected with pGCcoS3neo into LM(tk-), CHO and NIH3T3 cells. Cell lines selectively expressing the receptor (R85943) were used to screen cpds. for antagonist activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             treating benign prostatic hyperplasia prostate tissue
                                Briles DE,
                                                   20-MAR-1997.
16-SEP-1996; U14819.
15-SEP-1995; US-529055.
(UABR-) UAB RES FOUND.
                                                                                                                                                                                 /note- "unidentified WO9709994-A1.
                                                                                                                                                                                                                                                 /note= "unidentified amino Misc_difference 186
                                                                                                                                                                                                                                                                                                        Misc_difference 97
                                                                                                                                                                                                                                                                                                                                                                                                                                      Misc_difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-PSDB; T03128.
Use of selective alpha
      McDaniel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               04-APR-1995; U04203.
13-APR-1994; US-228932.
(SYNA-) SYNAPTIC PHARM CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R85943 standard;
R85943;
                                                                                                                                                                                                                                                                                                                                                                                                            /note-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note-
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NO9528157-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      oenign prostate hyperplasia.
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Alpha-1B adrenergic receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             452 alls1papeppgrrg-rhdsgp-lftfklltepes-pgtdggasng 494
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   isc_difference
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                                                                                                                                                                                                                                                                                                                                                                                                         "unidentified
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19; Conse
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   unidentified amino acid"
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   LS,
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larity 41.3%;
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larity 41.3%;
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a or inhibiting
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R66057
R66057;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This sequence shows the central portion, including the C-terminus of the alpha-hellx region and some of the proline-rich region, of pneumococcal surface protein A (FSPA) of Streptococcus pneumoniae strain Bg9163. Comparison of the N-terminal and central regions (W14533-57 and W14562-91) of PSPA polypeptides from different pneumococcal strains can be used to divide the strains into severa families based on sequence homologies. PSPA polypeptides, or fragments of them, can be used in vaccines to protect animals against S. pneumoniae infection and hence for the prevention of diseases such as otitis media, meningitis, bacteraemia and pneumon The sequence of the 3' half of the PSPA alpha-helical region and the immediate 5' tip of the coding sequence are likely to be the critical region and the control of the pspa alpha-helical region and the control of the coding sequence are likely to be the critical region.
                                                                                                                                                                                                                                                                                                                                                                       Claim 4; Page 34-38; 51pp; English.

A CDNA clone was obtd. (see T06027) from a HeLa cell cDNA library that encoded a novel density-enhanced Type III receptor-like PTP, designated hubEp-1 (R85203). hubEp-1 is useful for the study of PTPs and for the development of therapeutic or prophylactic cpds. e.g. for prevention of abnormal or malignant cell growth.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         09-NOV-1995.
03-MAY-1995; U05512
03-MAY-1994; US-237
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Example 6; Fig 13; 296pp; English.
This sequence shows the central portion, of the alpha-helix region and some of the
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                                                                                                                                                                                                                                                                                                                                                         Sequence
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Claim 4; Page 34-38; 51pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New density enhanced protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-PSDB; T06027
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W09530008-A1.
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                                                                                                                                   GVPAPLPPEDAPNAASLAPTPVSPVLEPFNLTSEP-SDYALDLSTFLQQHPAA
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                         standard;
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22; Conser
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Similarity 32.1%;
17; Conservative
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larity 31.4%;
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1. No. 1.53e+01;
Mismatches 31;
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1.53e+01;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PT Isolated DNA encoding a human N-methyl-D-aspartate receptor

PT subunit - used as probes in the identification and isolation of

PT nucleic acids encoding related receptor subunits.

PT nucleic acids encoding related receptor subunits.

PS Claim 11; Page 99-104; 156pp; English.

PS Claim 11; Page 99-104; 156pp; English.

PS CLAIM 11; Page 99-104; 156pp; English.

PS CLAIM 12; Page 99-104; 156pp; English.

PS CLAIM 13; Page 99-104; 156pp; English.

PS CLAIM 14; Page 99-104; 156pp; English.

PS CLAIM 15; Page 99-104; 156pp; English.

PS CLAIM 16; Page 99-104; 156pp; English.

PS CLAIM 17; Page 99-104; 156pp; English.

PS CLAIM 16; Page 99-104; 156pp; English.

PS CLAIM 17; Page 99-104; 156pp; English.

PS CLAIM 16; Page 99-104; 156pp; English.

PS CLAIM 17; Page 99-104; 156pp; English.

PS CLAIM 16; Page 99-104; 156pp; English.

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(SALK ) SALK INST BIOTECHNOLOGY IND ASSOC Daggett LP, Ellis SB, Liaw CW, Lu C; WPI; 94-341863/42.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note= "5 a.a. deletion of NMDAR2C a.a. sequence
between these residues"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     key Location/Qualifiers Misc_difference 591.592
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                                                                                                 27-OCT-1994.
20-APR-1994; U04387.
20-APR-1993; US-052449.
20-APR-1993; US-052449.
(SALK ) SALK INST BIOTECHNOLOGY IND ASSOC.
Daggett LP, Ellis SB, Liaw CW, Lu C;
WPI; 94-341863/42.
WPSDB; Q79372.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                06-JUL-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human N-methyl-D-aspartate receptor subunit 2C protein. N-methyl-D-aspartate; receptor; human; NMDA; cation-selective; channel; glutamate; hippocampus; rat; pcDNAl; NMDA receptor; antagonist.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20-APR-1994;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R66062 standard;
                                    Isolated DNA encoding a human N-methyl-D-aspartate receptor subunit - used as probes in the identification and isolation of
                                                                                                                                                                                                                                                                                                                                                                                             WO9424284-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            05-JUL-1995 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R66037;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R66037 standard; Protein; 1236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                924 apppspcptprsgpspclptpdpppepsptgwgppdggra 963
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         dentify compounds which bind
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TPAPSTIPGPRRGSGPEIFTFDPLPEPAAAPAGRPSASRG 57

    used as prol
acids encoding

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1231 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          42.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 96;
Pred. No.
11; Misma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             or are antagonistic to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      B
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. 1.78e+01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12;
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Query Match
Best Local S
Matches 1

Local Similarity les 17; Conser

42.5%;

Score 96;

Pred.

No. 1.78e+01; Mismatches 12;

DB 12;

Length 1239;

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CC (NMDAR2C). The NMDA receptor contains two subunits: subunit R1

CC (Q79370) and subunit R2 selected from the subunits 2A (Q79375), 2B

CC (Q79377), 2C and 2D (Q79378). The receptor forms part of a family of

CC (Q79377), 2C and 2D (Q79378). The receptor forms part of a family of

CC NMDA receptors which have cation-selective channels and bind glutamate

CC and NMDA. The NMDAR2C gene was obtained by amplifying cDNA derived from

CC human brain tissues with primers corresponding to sequences in the rat

CC NMDAR2A receptor DNA and using the resultant fragments as probes to

CC screen a cDNA library derived from human hippocampal RNA. 4 basic clones

CC were isolated: NMDAR2 (Q79399), NMDAR2 (Q7940), NMDA24 (Q79401) and

CC NMDAR26 (Q79402). The clones are thought to be splice variants of each

CC (Q79403-7) of the NMDAR2C receptor were constructed. The expression of

CC (Q79403-7) of the NMDAR2C receptor were constructed. The expression of

CC the genes allows the reconstruction of the NMDAR receptor. The complete

CC to the human NMDA receptor.
PT Isolated DNA encoding a human N-methyl-D-aspartate receptor provided DNA encoding related receptor subunit.

PT subunit - used as probes in the identification and isolation of provided acids encoding related receptor subunits.

PS Claim 11: Page 99-104: 156pp; English.

PS Claim 11: Page 99-104: 156pp; English.

CC (NMDAR2C) gene clone NMDAR2C-delta15-124. This clone covers the same companies of the novel N-methyl-D-aspartate (NMDA) receptor companies and insertion of a.a. 591-5 and an insertion of 8 a.a. between a.a. 721-2 of the NMDAR2C protein companies of variants (079403-7) of the NMDAR2C protein constructed, by recombination, based on the sequence of the 4 basic clones: NMDA21 (079399), NMDA22 (079400), NMDA24 (079401) and NMDA26 (079402). The NMDA receptor contains two subunits: subunit R1 (079370) cand subunit R2 selected from the subunits 2A (079375), 2B (079377), 2C cand 2D (079378). The receptor forms part of a family of NMDA receptors which have cation-selective channels and bind glutamate and NMDA. The expression of the genes allows the reconstruction of the NMDA receptor. CT he complete receptor can be used to identify compounds which bind or are antagonistic to the human NMDA receptor.
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human NMDAR2 receptor subunit clone NMDAR2C-delta15-I24 protein N-methyl-D-aspartate; receptor; human; NMDA; cation-selective; glutamate; hippocampus; rat; pcDNA1; NMDA receptor; antagonist
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note= "5 a.a deletion o
between these residues "
Misc_difference 717 . 723
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Key Location/Qualifiers Misc_difference 591.592
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               06-JUL-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                          20-APR-1993; US-052449.
(SALK ) SALK INST BIOTECHNOLOGY IND ASSOC.
Daggett LP, Bllis SB, Liaw CW, Lu C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20-APR-1994; U04387
20-APR-1993; US-052
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "8 a.a.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     h 8.6%;
Similarity 42.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1236 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Protein; 1239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            of NMDAR2C a.a. sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 96; DB 12;
Pred. No. 1.78e+01;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
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Claim 11; Page 99-104; 156pp; English.

CC The nucleotide sequence of the novel N-methyl-D-aspartate (NMDA) receptor CC (NMDAR2C) gene clone pCMV-26-ScaI-24. This clone covers the same CC sequence as the NMDAR2C sequence and contains an insertion of 8 a.a. CC between a.a. 722-8 of the NMDAR2C protein (R66035). A series of variants (C 279403-7) of the NMDAR2C receptor were constructed, by recombination, CC based on the sequence of the 4 basic clones: NMDA21 (079399), NMDA22 (079400), NMDA24 (079401) and NMDA26 (079402). The NMDA receptor CC contains two subunits: subunit R1 (079370) and subunit R2 selected from CC the subunits 2A (079375), 2B (079377), 2C and 2D (079378). The receptor CC channels and bind glutamate and NMDA. The expression of the genes allows CC used to identify compounds which bind or are antagonistic to the human CC unda receptor.
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Best Local
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                                                                                                              /label= apoE4 homology
Cleavage_site 43..44
Cleavage_site 182..183
Misc_difference 3
     /label= kinase c phosphorylation site Misc_difference 42 /label= kinase c phosphorylation site Misc_difference 43 /label= kinase c phosphorylation site
                                                                                                                                           Cleavage_site
Cleavage_site
Misc_difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NMDA receptor.
Sequence 1244 AA;
                                                                                                                                                                                                                                                                                          Domain
                                                                                                                                                                                                                                                                                                                                                                              ApoE4L protease
ApoE4L; proteas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R59841 standard; Protein; 198 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-PSDB; Q79403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (SALK) SALK INST BIOTECHNOLOGY IND ASSOC Daggett LP, Ellis SB, Liaw CW, Lu C; WPI; 94-341863/42.
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                                                                                                                                                                                                                                                                                                                                                Homo sapiens.
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20-APR-1994;
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                                                                                                                                                                                                                                                                                                                                                                                                                          26-JAN-1995 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18 TPAPSTIPGPRRGSGPEIFTFDPLPEPAAAPAGRPSASRG
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Similarity 42.5%;
17; Conservative
                                                                                                                                                                                                                                                                                                                                                            protease; enzyme; Alzheimer disease; diagnostic; therapeutic
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                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
phosphorylation site
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Pred. No.
11; Misma
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. 1.78e+01;
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B
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Best Local S
Matches 1
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Misc_difference 87
/label= kinase c.phosphorylation s:
Misc_difference 112
/label= kinase c phosphorylation s:
Misc_difference 129
                                                                                    Claim 22; Page 39-40; 72pp; English.

ApoB4L is a protease catalyzing the formation of the abnormal beta/Avariant of beta-amyloid protein, and is used to develop an inhibitor for the diagnosis and teatment of Alzheimer disease, Downs syndrome, Parkinson disease, schizophrenia, hyperlipoproteinemia or
                                                                                 cardiovascular
                                                                                                                                                       New proteinase esterase-like proteins - used to develop for the diagnosis and treatment of Alzheimer's disease a related diseases
                                                                                                                                                                                             WPI; 94-234212/28.
P-PSDB; Q69099.
                                                                                                                                                                                                                                                        23-JUN-1994.
16-DEC-1993; E03581.
16-DEC-1992; CA-085924.
04-MAR-1993; US-291401.
                                                                                                                                                                                                                                                                                                                                   /label= kinase c phosphorylation
Misc_difference 129
                                                                                                                                                                                                              Bergmann JE,
WPI; 94-2342
                                                                                                                                                                                                                                 (BERG/) BERGMANN J E
                                                                                                                                                                                                                                                                                                             WO9413798-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                       Misc_difference 54
                                                                                                                                                                                                                                                                                                                        /label= kinase c
                    h 8.5%;
Similarity 43.2%;
16; Conservative
                                                                     198 AA;
                                                                                                                                                                                                                       Preddie RE
                                                                                  disease.
                                                                                                                                                                                                                                                                                                                        phosphorylation
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                    Score 95;
Pred. No.
5; Misma
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                    Mismatches 15;
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                                DB 10;
2.06e+01
                                                                                                                            of the abnormal beta/A4
                                            Length 198
                    Indels
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                   Gaps
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Search completed: Fri Apr Job time : 24 secs. Q 40 73 pareptvaartrpcstrgpr-rsrmalrprsapsrap 108 PLPEPAAAPAGRPSASRGHRKRSRRVLYPRVVRRQLP 17 13:41:26 1998 76

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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Tabular output not generated. Fri Apr 17 13:40:06 1998; MasPar time 10.54 Seconds 633.960 Million cell updates/sec

Title: >US-08-799-910-10 (1-156) from US08799910.pep

Description: Perfect Score:

Sequence: 1114
1 MCHSRSCHPTMTILQAPTPA.....EPSDYALDLSTFLQQHPAAF

Scoring table: PAM 150 Gap 11

195121 seqs, 42852602 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

pir55 1:pir1 2:pir2 3:pir3 4:pir4

Database:

Statistics: Mean 36.831; Variance 125.421; scale 0.294

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

11 13 14 14 15 16 11 18 19 20 20 21 23	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	Result No.
103 101 101 100 100 100 98 98 98 98	1111 152 1752 117 114 1109 109 102 103 103	Score
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1468 268 416 816 333 439 1492 272 272 272 351 351 390 475	156 153 474 351 228 1729 1753 913 1106	Length I
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3.00e+00 4.49e+00 4.49e+00 5.49e+00 5.49e+00 6.70e+00 8.17e+00 8.17e+00 8.17e+00 8.17e+00	8.18e-119 1.10e-74 1.63e-01 3.09e-01 7.13e-01 8.78e-01 3.67e+00 3.67e+00 3.67e+00	Pred. No.

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ALIGNMENTS

δõ В δÃ 밁 Ş 멍 Query Match 99.7%; Score 1111; DB 2; Best Local Similarity 99.4%; Pred. No. 8.18e-119; Matches 155; Conservative 1; Mismatches 0; JC5537 A;Experimental source: monocyte A;Note: the authors translated the codon CCG for residue 106 as Arg SEQUENCE 156 AA; 16914 MW; 127043 CN; This is a DE line. 01-JAN-1900 XXXXXX 121 121 APTPVSPVLEPFNLTSEPSDYALDLSTFLQQHPAAF APTPVSPVLEPFNLTSEPSDYALDLSTFLQQHPAAF 156 STANDARD; PRT; 156 AA 156 Length 156; Indels 0; Gaps 0

RESULT 2 ID S33363 Query Match Best Local Similarity This is a DE line. 01-JAN-1900 XXXXXX A;Cross-references: EMBL:X67644 C;Genetics: A;Introns: 70/3 A;Keywords: transmembrane protein C;Keywords: transmembrane protein STANDARD; 67.5%; 70.6%; EMBL: X67644 PRT; Score 752; DB 2; Pred. No. 1.10e-74; 153 AA Length 153;

PID: 9332564

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                                                                                                        349 TPTPTPTPTPTPTPTPTYDITYVVF-DVTPSPTPTPTPTPTPTPTPTPTPTPTPTP 405
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A:Residues: 207-474 <NEW>
A:Cross-references: EMBL:X14717
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                                                                                                                                                                                                                                                                                                                                                                                            R; Neumann, H.; Zillig, W.
Nucletc Acids Res. 18, 2171, 1990
A;Tille: Nucleotide sequence of the viral
A;Reference number: S15921; MUID:90245666
A;Accession: S15921
                                                                                                                                                                                                                                                                                                                                         A; Note: the authors translated
                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: DNA
A; Residues: 1-474 <NEU>
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les 28; Conser
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A: Variety: strain KRA1 10/1
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                                                                                    RVVRRQLPVEEPNPAKRLLFLLLTIVFCQILMAEEGVPAPLPPEDAPNAASLAPTPVS
                                                                                                                             PTMTILQAPTPAPSTIPGPRRGSGPEIFTFDPLPEPAAAPAGRPSASRGHRKRSRRVLYP 68
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Pred. No. 1.63e-01;
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                                                                                                                                              A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-228 <ABJ
SEQUENCE 228 AA; 2248
                                                                                                                                                                                     R;Abrahams, S.; Hayes, C.M.; Watson, J
Plant Mol. Biol. 27, 513-528, 1995
A;Tille: Expression patterns of three
A;Reference number: $53504
A;Accession: $53504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: GB:M30023;
SEQUENCE 351 AA; 39888 MW; 427
154 SSPPA
                                                                                                                                                                                                                                                    C:Species: Medicago sativa (alfalfa)
C:Date: 15-Jul-1995 #sequence_revision 03-Nov-1995
                                                                                                                                                                                                                                                                           extensin-like protein S3 - alfalfa
                                                                                                                                                                                                                                                                                         >P1;S53504
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                     76
                                         95
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A;Title: Sequence analysis of A;Reference number: A34768;
                                                             16
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A; Residues: 1-351 <FRA>
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R; Fraser, K.M.; Hil
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C:Species: Orf virus
C:Date: 23-Aug-1991 #sequence_revision
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                                  PVQQSPPPTPLTPPPVQST-PPPASPPPASPPPFSPPPATPPPATPPPATPPPALTPTPL 153
                                                        APTPAPSTIPGPRRGSGPEIFTFDPLPEPAAAPAGRPSASRGHRKRSRRVLYPRVVRRQL
                                                                            PPTPPANTPPTTPQASPPPVQS-SPPPVQSSPPPVQSSPPPAQSTPPPVQSSPPPVSAPP
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13-528, 1995
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Pred. No. 7.13e-01;
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A;Molecule type: mRNA
A;Residues: 1-753 <br/>CIN>
A;Experimental source: strain Jervis Bay isolate<br/>SEQUENCE 753 AA; 82427 MW; 3187938 CN;
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                                                                                                                                                                                                                                                                                                                                                                  328
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exo-alpha-sialidase (EC 3.2.1.18) -
                      >P1;S20590
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                                                              TOIG of: s20590
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31; Conservative
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larity 32.9%;
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Pred. No. 8.78e-01;
30; Mismatches 65
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Pred. No. 3.67e+00;
14; Mismatches 30;
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C;Date: 22-Nov-1993 #sequence_revision 01-Dec-1995 #text_change 09-Sep-1997
                                                                                                           This is a DE line
                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Molecule type: DNA
A;Residues: 1-1106 <SHI>
A;Residues: 1-1106 <EMBL:X15867
A;Cross-references: EMBL:X15867
A;Note: all the codons between two in-frame stop codons are translated; the A;Note: the gene encoding this protein overlaps uvra gene
SEQUENCE 1106 AA; 119484 MW; 4705861 CN;
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Biol. Chem. Hoppe-Seyler 372, 1065-1072, 1991
A;Title: Cloning, sequencing and expression o
A;Reference number: S20590; MUID:92162190
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A; Residues: 1-913 <HEI>
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   >P1;S24407
formin isoform IV - mouse
C:Species: Mus musculus (house mouse)
C:Date: 19-Feb-1994 #sequence_revision
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Pred. No. 3.67e+00;
16; Mismatches 29
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Pred. No. 3.00e+00
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S11515
                        A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-268 <KAG>
A:Cross-references: GB:M65149; NID:g203411;
SEQUENCE 268 AA; 28600 MW; 338810 CN;
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A;Residues: 1-1468 <WOY>
A;Cross-references: EMBL:X53599; NID:g52877; PID:g52878
SEQUENCE 1468 AA; 163808 MW; 11493196 CN;
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A;Title: A variant limb deformity transcript expressed A;Reference number: $24407; MUID:92112033
A;Molecule ****
                                                                         A; Accession: B39429
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(;Species: Mus musculus (house mouse)
C;Date: 22-Jan-1994 #sequence_revision
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A;Residues: 1-1206 <JAC>
A;Cross-references: EMBL:X62379; NID:g51552;
SEQUENCE 1206 AA; 133463 MW; 7742033 CN;
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Score 101;
Pred. No. 4
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Pred. No. 3.00e+00;
15; Mismatches 9
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Pred. No. 3.00e+00;
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A;Gene: qa-lF
C;Superfamily:
                                                                R;Geever, R.F.; Huiet, L.; Baum, J. Mol. Biol. 207, 15-34, 1989 A;Title: DNA sequence, organizat. A;Reference number: S04250; MUID A;Accession: S04256
                                                                                                                    regulatory protein qa-1F - Neurospora c
N;Alternate names: QA activator
C:Species: Neurospora crassa
C:Date: 26-Apr-1989 *sequence_revision
C:Accession: S04256; F31277
                       C; Genetics:
                                 A; Cross-references:
                                             A; Molecule type: I
A; Residues: 1-816
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-JAN-1900
                                                                                                                                                                                                                                                                                                                                               353 ALLSLPAPQPPGRRG-RRDSGP-LFTFRLLAERGSPAAG
                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: mRNA
A; Residues: 1-417 <LT5>
A; Cross-references: GB: X14050; NID: g902; PID: g833784
C; Superfamily: vertebrate rhodopsin
C; Keywords: G protein-coupled receptor; glycoprotein
SEQUENCE 417 AA; 45891 MW; 865241 CN;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    alpha-1-adrenergic receptor - dog (fragment)
C:Species: Canis lupus familiaris (dog)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Status: nucleic acid sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Title: Selective amplification and cloning A; Reference number: A30341; MUID:89242119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R; Libert, F.; Parmentier, Science 244, 569-572, 1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Date:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              142 CAQTVVSLAAAAQPTPPTSPEPPRGSPGPSLAP-GPVREKGAGKRGPDRGSPEYRQRRER 200
                                                                                                                                                                                                                                                                                                                            12 TILQAPTPAPSTIPGPRRGSGPEIFTFDPLPEPAAAPAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;Species: Canis tupus tum----;Date: 31-Dec-1990 #sequence_revision
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                                   EMBL:
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Pred. No. 4.49e+00;
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65241 CN;
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                              NID: 93060; PID: 93068
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unassigned GAL4-type zinc cluster proteins; GAL4 zinc binuclea.

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RESULT 15
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Search completed: Fri Apr 17 13:40:43 1998 Job time : 37 secs.
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Best Local Similarity 33.3%;
Matches 16; Conservative
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Best Local Similarity 34.0%;
Matches 16; Conservative
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SEQUENCE 333 AA; 36351 MW; 508377 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              This is a DE line.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Keywords: DNA binding; nucleus; transcription regulation; zinc F;71-108/Domain: GAL4 zinc binuclear cluster homology <GAL4> F;76-103/Region: zinc binding #status predicted F;773-793/Domain: transcription activation #status predicted <TAN> SEQUENCE 816 AA; 88946 MW; 3481791 CN;
                                                                                                                                                                                                                                                                                       A;Accession: S61849
A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-333 <VAN>
A;Cross-references: EMBL:Z14056; NID:g550397; PID:g550401
A;Cross-references: EMBL:Z14056; NID:g550397; PID:g550401
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 408 VVRTQLPPDDDRPRPRMRALLVACFIVDTIVSMRHNVPAHLKPDDIAD 455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        70 VVRRQLPVEEPNPAKRLLFLLTIVFCQILMA-EEGVPAPLPPEDAPN 116
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29 RGSGPEIFTFDPLPEPAAAPAGRPSASRG-HRKRSRRVLXPRVVRRQ 74
                                                                                                         3 RITGPSSAIY-TLPDPATTPAQPAAATPNTHRRRPRQ-LHEREIEHE 47
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Pred. No. 4.49e+00;
13; Mismatches 18; Indels
                                                                                                                                                                   Score 100; DB 2; Length 333;
Pred. No. 5.49e+00;
14; Mismatches 14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             333 AA.
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Release 3.0.4A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1997 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Tabular output not generated. Fri Apr 17 13:39:01 1998; MasPar time 12.21 Seconds 538.123 Million cell updates/sec

Title:

Description: Perfect Score:

Scoring table:

PAM 150 Gap 11

Searched:

140555 seqs, 42109429 residues

Sequence: >US-08-799-910-10 (1-146) from US08799910.pep 1 MCHSRSCHPTMTILQAPTPA.....EPSDYALDLSTFLQOHPAAF 156

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

sptremb15
1:sp_fung1 2:sp_human 3:sp_invertebrate 4:sp_mammal
5:sp_mhc 6:sp_organelle 7:sp_phage 8:sp_plant
9:sp_bacteria 10:sp_rodent 11:sp_virus 12:sp_vertebrate
13:sp_unclassified

Statistics: Mean 42.617; Variance 98.163; scale 0.434

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

1 5 5 5 6 7 7 7 8 8 8 7 1 1 1 1 1 1 1 1 1 1 1 1 1	Result
1114 112 112 112 111 110 110 110 100 100 100	Score
100.0 100.2 100.1 100.1 100.0 9.9 9.2 9.2 9.2 9.2 9.2 9.3 9.0	Query Match Length
156 155 115 1285 285 2285 2285 2285 2285 22	Length
111 111 111 111 111 111 111 110 110 110	BG
Q92691 P983006 P78977 Q65553 Q65553 Q65553 Q6343 Q96343 Q96343 Q963171 Q983187 Q983187 Q98311 P96311 P96311 P96311 P96311 P96311 Q42421 Q42421 Q42421 Q634627 Q634627	ID
PRG1 PROTEIN (DIF-2 PR HOMOLOGUE OF RETROVIRA PREDICTED ORF. CELL WALL PROTEIN PREC UL36. GENOME RICH PROTEIN PROTEINE PROLINE RICH PROTEIN PROLING PROSINIASE-BINDING PROSINILAR TO CUTICULAR CARTICULIN P60. ARTICULIN P60. ARTICULIN P60. VACCINA VIRUS GENE F1 MC018L. SIALIDASE (EC 3.2.1.18 ENDOGLUCANASE A (EC 3.2.1.18 CUT-LIKE 2 (CUX-2). PUTATIVE PROLINE-RICH HRPV. CHITINASE PRECURSOR. CTD-BINDING SR-LIKE PR ALPHA-1 TYPE II' COLLA	Description
8.46e-174 3.65e-02 3.65e-02 3.65e-02 3.65e-02 4.84e-02 6.41e-02 6.41e-02 5.74e-01 5.74e-01 5.74e-01 5.74e-01 5.74e-01 5.74e-01 5.74e-01 5.74e-01 5.74e-01 5.74e-01 5.74e-01 5.74e-01 5.74e-01 5.79e-01 9.79e-01 9.79e-01 9.79e-01 9.79e-01	Pred. No.

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MOB3 ORF. F47B8.5.	(VSP-3) PRECURSOR.	OLEOSIN.	R11A8.7 (FRAGMENT).	GABA/NORADRENALINE TRA	CHITINASE PRECURSOR.	3-PHOSPHOINOSITIDE DEP	MLO PROTEIN.	CAPSID SCAFFOLD PROTEI	ZEIN.	N-METHYL-D-ASPARTATE R	WIP1.	BMP4.	FORK HEAD PROTEIN.	HYPOTHETICAL 40.2 KD P	ALR.	ALR.	PROTEIN-TYROSINE PHOSP	GENOME, PARTIAL SEQUEN	BACTINECIN 11.	ALPHA-1 TYPE II COLLAG	WP6 PRECURSOR.	(FRAGMENT).	BETA-GLUCOSIDASE.
4.67e+00	4.67e+00	4.67e+00	3.61e+00		٠	3.61e+00	•	3.61e+00	٠			2.79e+00	٠	2.79e+00	2.15e+00		2.15e+00	2.15e+00	٠		1.66e+00	1.28e+00	1.28e+00

ALIGNMENTS

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121 APTPVSPVLEPFNLTSEPSDYALDLSTFLQQHPAAF 156 	61 RSRRVLYPRVVRRQLPVEEPNPAKRLLFLLTIVFCQILMAEEGVPAPLPPEDAPNAASL 120 	1 MCHSRSCHPTMTILQAPTPAPSTIPGPRRGSGPEIFTEDPLPEPAAAPAGRPSASRGHRK 60 	Query Match 100.0%; Score 1114; DB 2; Length 156; Best Local Similarity 100.0%; Pred. No. 8.46e-174; Matches 156; Conservative 0; Mismatches 0; Indels 0; Gaps	SEQUENCE 156 AA; 16928 MW; 46013510 CRC32;	EMBT: Y06438: E350480: -:	CANCER RES. 56:1498-1502(1996).	KONDRATYEV A.D., CHUNG K.N., JUNG M.O.;		BIOPHYS. RES. COMMUN. 235:4-9(1997).	DIETZSCH A. BUECHLER C., ASLANIDIS C., SCHMITZ G.;	(2)	SUBMITTED (MAR-1996) TO EMBL/GENBANK/DDBJ DATA BANKS.	TRAUZOLD A.;	SEQUENCE FROM N.A.		EUKARYOTA; METAZOA; CHORDATA; VEKTEBKATA; TETKAPODA; MAMMADIA; EUTHERIA; PRIMATES:	SAPIENS (HUMAN).	\sim	TEIN (DIF-2 PROTEIN).	998 (TREMBLREL. 05, LAST ANNOTATIO	O1-FEB-1997 (TREMBURED: 02, CREATED)	092691 PRELIMINARY; PRT; 156 AA.	

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MEDLINE; 90266454

FRASER M., HILL D.F., MERCER A

VIROLOGY 176:379-389(1990).

EMBL; M30023; G332564; SEQUENCE 351 AA; 39888 MW;
                                                                                                                                                                                                                                                                                           TYAGI J.S.
SUBMITTED
                                                                                                                                                                    SEQUENCE
                                                                                                                                                                          TYAGI J.S.;
SUBMITTED (FEB-1996) TO EMBL/GENBANK/DDBJ DATA
EMBL; X63508; E282228; -
                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
STRAIN-H37RV;
TYAGI J.S.;
                                                                                                                                                                                                                                                                                                                                            PREDICTED ORF.
MYCOBACTERIUM TUBERCULOSIS.
PROKARYOTA; FIRMICUTES; ACT
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01-MAY-1997 (TREMBLREL.
01-MAY-1997 (TREMBLREL.
01-MAY-1997 (TREMBLREL.
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Q85302;
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PARAPOXVIRUSES.
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01-NOV-1996 (TREMBLREL.
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NDIAN J. BIOCHEM. BIO
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24; Conser
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larity 25.4%;
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llarity 32.9%;
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BIOPHYS. 32:429-436(1995)
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. PSEUDOPROTEASE.
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                                                                                                                                                                                                                                                                                         EMBL/GENBANK/DDBJ
                                                                                                                                                                                                                                                                                                                                          ACTINOMYCETALES; MYCOBACTERIACEAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VIRUSES; POXVIRIDAE; CHORDOPOXVIRINAE;
                                                                                                                      Score 112; DB 9; Le
Pred. No. 3.65e-02;
23; Mismatches 22;
                                                                                                                                                                                                                                                                                                                                                                        CREATED)
LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 114; DB 11;
Pred. No. 2.07e-02;
12; Mismatches 35
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LAST ANNOTATION UPDATE)
 PRT;
                                                                                                                                                                 AF306566 CRC32;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8EEF741B CRC32;
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                                                                                                                                          Length 115
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RAPERA REPRESENTATION OF THE REPRESENTATION 
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Best Local Similarity
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Q65553;
Q1-NOV-1996
Q1-NOV-1996
Q1-JAN-1998
                                                                                                                                        SCHWYZER M.,
LABOISSIERE (
                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. STRAIN-COOPER;
                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN-COOPER;
SCHWYZER M., STYGER D., VOGT
LABOISSIERE S., MISRA V., VL
VET. MICROBIOL. 0:0-0(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  UL36.
                                                                                                                                                                                          STRAIN-JURA;
                                                                                                                                                                                                                     SEQUENCE OF 1-179 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SCHWYZER M., VLCEK C
THIRY E., PACES V.;
SUBMITTED (AUG-1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BOVINE HERPESVIRUS TYPE 1.
VIRIDAE; DS-DNA ENVELOPED VIRUSES;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            UL36.
                                 STRAIN-JURA;
                                                                                                               VET. MICROBIOL.
                                                                                                                                                                                                                                                                     SUBMITTED (AUG-1996) TO EMBL/GENBANK/DDBJ
                                                                                                                                                                                                                                                                                                   SCHWYZER M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                             SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE OF 1-179 FROM
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YEAST 12:1535-1548(1996).
EMBL: Z81006; E274837; -.
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01-MAY-1997 (TREMBLREL 03, CREATED)
01-MAY-1997 (TREMBLREL 03, LAST SEQUENCE UPDATE)
01-JAN-1998 (TREMBLREL 05, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN-CX39-74A; T
MEDLINE; 97127825.
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YARROWIA LIPOLYTICA (CANDIDA LIPOLYTICA)
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SEQUENCE FROM N.A.
TISSUE-PINA240;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (TREMBLREL.
                                                                                                            STYGER D., VOGT B.
S., MISRA V., VLCEK
OL. 53:67-77(1996).
        VLCEK
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llarity 28.5%;
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     LOWERY
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01,
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LAST SEQUENT ANNOTATION AND LAST ANNOTATION AND LAST AND 
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Pred. No. 3.1
29; Mismatcl
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  D.E.,
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                                                                                                                                     LOWERY D.
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ANNOTATION UPDATE)
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BELLO L.J.,
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.65e-02;
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RESULT CONTROL OF THE                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Š
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Best Local S
Matches 2
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01-NOV-1996
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Q84630;
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EMBL; 278205; E258467
EMBL; AJ004801; E1187
SEQUENCE 3247 AA;
                                                                                                                                                                                                                                                       Q43558
Q43558,
01-NOV-1996 (TREMBLREL 01,
01-NOV-1996 (TREMBLREL 01,
01-NOV-1996 (TREMBLREL 01,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
MEDLINE: 95133167.
MEDLINE: 95133167.
LU Z., LI Y., ZHANG Y., KUT.
VIROLOGY 206:339-352(1995).
EMBL: U42580; G1181479; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN-JURA;
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VIRIDAE; DS-DNA NONENVELOPED VIRUSES;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENOME, PARTIAL
  SIGNAL;
                                    STRAIN-CV. SIRIVER; TISSUE-STEM;
MEDLINE; 95201245.
ABRAHAMS S., HAYES C.M., WATSON J.;
PLANT MOL. BIOL. 27:513-528(1995).
EMBL; L36120; G535586; -.
                                                                                                                                                                                                                  PROLINE RICH PROTEIN PRECURSOR. MEDICAGO SATIVA (ALFALFA).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                  EUKARYOTA;
                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                               FABACEAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                           149 HDLP 152
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           L-PAAQPRQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PTMTILQAPTPAPSTIPGPRRGSGPEIFTFDPLPEPAAAPA-GRPSASRGHRKRS--RRV
                                                                                                                                                                                                                                                                                                                                                                                                                   RQLP 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APTPAPSTIPGPRRGSGPEIFTFDPLPEPAAAPAGRPS-ASRGHRKRSRRV-LYPRV-VR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
23; Conser
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26; Conse
      STRUCTURAL PROTEIN.
1 7
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                                                                                                                                                                                                  PLANTA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (TREMBLREL. (TREMBLREL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          225 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10.0%;
larity 37.7%;
Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                    EMBRYOPHYTA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9.98;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL/GENBANK/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KUTISH
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11; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 111; DB 11,
Pred. No. 4.84e-02;
28
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LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                         CREATED)
LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
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Pred. No. 6.41e-02;
14; Mismatches 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                           PRT;
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                                                                                                                                                                                                    ANGIOSPERMAE;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 28;
                                                                                                                                                                                                    DICOTYLEDONEAE; FABALES;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     225;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4;
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RAARA SSCATA
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Best Local S
Matches
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Best Local S
Matches 2
                                                                                                                                                                                        LT 8
Q96343
Q96343;
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SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; U59446;
NON_TER
SEQUENCE 552
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EUKARYOTA; P
CAPPARALES;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-FEB-1997 (TREMBLREL. 02, CREATED 01-FEB-1997 (TREMBLREL. 02, LAST SE 01-FEB-1997 (TREMBLREL. 02, LAST AN MYROSINASE-BINDING PROTEIN RELATED BRASSICA NAPUS (RAPE).
EUKARYOTA; PLANTA; EMBRYOPHYTA; ANG
WILSON R., AINSCOUGH R., ANDERSON K., BAXNES C., BERKS M.,
BONFIELD J., BURTON J., CONNELL M., COPSEY T.,
COULSON A., CRAXTON M., DEAR S., DU Z., DURBIN R., FAVELLO A.,
FULTON L., GARDNER A., GREEN P., HAWKINS T., HILLIER L., JIER M.,
JOHNSTON L., JONES M., KERSHAW J., KIRSTEN J., LAISTER N.,
LATREILLE P., LIGHTNING J., LLOYD C., MCHURRAY A., MORTIMORE B.,
O'CALLAGHAN M., PARSONS J., PERCY C., RIFKEN L., ROOPRA A.,
SAUNDERS D., SHOWNKEEN R., SMALDON N., SMITH A., SONNHAMMER E.,
STADEN R., SULSTON J., THIERRY-MIEG J., THOMAS K., VAUDIN M.,
VAUGHAN K., WATESSTON R., WATSON A., WEINSTOCK L.,
WATENSTON R., WATSON A., WEINSTOCK L.,
WHILKINSON-SPROAT J., WOHLDMAN P.;
                                                                                                                                                                                                                                                                      O01662
                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN-20516 OF SVALOFS TAIPALENSUU J., FALK A., SUBMITTED (NOV-1996) TO
                                                                                                                             STRAIN-BRISTOL N2;
MEDLINE; 94150718.
                                                                                                                                                                                      CAENORHABDITIS
                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                           EUKARYOTA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                135
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                                                                                                                                                                                                                                                                                                                    14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 36 PPTPPANTPPTTPQASPPPVQS-SPPPVQSSPPPVQSSPPPAQSTPPPVQSSPPPVSAPP
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                                                                                                                                                                                                                                                                                                                                      LRTPAPAPSPAPGPAPAPAPGSHP-APAPAPAPAPGQGPRPAPAPG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SSPPA 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PVEEPNPAKRLLFLLLTIVFCQILMAEEGVPAPL-PPEDAPNAASLAPTPVSPVLEPFNL
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                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         30;
                                                                                                                                                                                                                                                                                                                                                                20;
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                                                                                                                                                                         TIS ELEGANS.
METAZOA; ACOELOMATES;
                                                                                                                                                                                                                                                                                                                                                                                                              552 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CRUCIFERAE
                                                                                                                                                                                                                                                                                                                                                               9.7%;
larity 43.5%;
Conservative
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                                                                                                                                                                                                                                                                       PRELIMINARY;
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22480
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBRYOPHYTA; ANGIOSPERMAE; DICOTYLEDONEAE;
                                                                                                                                                                                                                                                                                                                                                                                                              59270 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          KARAT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     02, CREATEU)
02, LAST SEQUENCE UPDATE)
02, LAST ANNOTATION UPDATE)
771 PFLATED PROTEIN (FRAGMENT).
                                                                                                                                                                                                                     04, CREATED)
04, LAST SEQUENCE UPDATE)
04, LAST ANNOTATION UPDAT
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Pred.
11; M
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pred. No. 6.41e-02;
36; Mismatches 56
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                6861EF25 CRC32;
                                                                                                                                                                                                                                                                                                                                                                  Mismatches 12;
                                                                                                                                                                              NEMATODA;
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O
                                                                                                                                                                                                                                                                                                                                                                           108; DB 8;
No. 1.12e-01;
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                                                                                                                                                                              SECERNENTEA;
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                                                                                                                                                                              RHABDITIDA.
                                                                                   JIER M.,
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Best Local S
Matches 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local S
Matches 2
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WATERSTON R.;
SUBMITTED (APR-1997) TO EMBL
SUBMITTED (APR-1997) TO EMBL;
EMBL; AF000198; G2047346; -
EMBL; AF000198; G2047346; -
EMBL; AF000198; G2047346; -
                                                                                                                                                                                        01-NOV-1996 (TREMBLREL. (
01-NOV-1996 (TREMBLREL. (
01-MAY-1997 (TREMBLREL. (
VACCINIA VIRUS GENE F12L
                                                                                                                                                                                                                                                                                        LT 11
Q84171
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01-NOV-1996 (
                                                        STRAIN-NZ2;
MERCER A.A.;
                                                                                                                                                    ORF VIRUS:
VIRIDAE; DS-DNA
                                                                                                                                                                                                                                                  Q84171;
01-NOV-1996
SEQUENCE FROM N.A
                                                                                              SEQUENCE FROM N.A.
                                      SUBMITTED (OCT-1995)
                                                                                                                                  PARAPOXVIRUSES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q27212
Q27212;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN-N5B;
MEDLINE; 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ARTICULIN P60.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN-BRISTOL N2;
MADSEN C., FRONICK B.;
SUBMITTED (APR-1997) T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NASSULIDA.
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STRAIN-BRISTOL N2;
                                                                                                                                                                                                                                                                                                                                                                                             391 HVPIPHDVPVAQEVIVQQPFAVPQPYTVQQEVPIPHPVPVPQPYAVP-QPVPVPTPVAVP 449
                                                                                                                                                                                                                                                                                                                                                                                                                                                             332 VNVPVDVPIEVPVPVDRDVPVPFQLN-IDVPVDVPVARPVEVERIIQQPIPLEQPRLVEQ
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[2]
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           363 AAAGAAAPPPAPAAAAAAPEPAP-APAAAPPPAPAAGGSDTGGYRRKKVRRVL--RIVR 417
                                                                                                                                                                                                                                                                                                                                                                     74
                                                                                                                                                                                                                                                                                                                                                                                                                                       14 LQAPTPAPSTIPGPRRGSGPEIFTFDPLPEPAAAPAGRPSASRGHRKRSRRVLYPRVVRR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CELL BIOL. 130:1401-1412(1995).
3L; L41557; G767685; -.
                                                                                                                                                                                                                                                                                                                                                           QLPVEEPNPAKRLLFLLTIVFCQILMAEEGVPAPLP-PEDAPNAASLAPTPV-SPVLEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
30; Conser
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22; Conse
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           568 AA; 61110 MW; CA5BB376 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9.2%;
llarity 25.0%;
Conservative
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                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                    ENVELOPED
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GEISLER N.,
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                                  EMBL/GENBANK/DDBJ
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                                                                                                                                                    VIRUSES;
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                                                                                                                                                                                                      , CREATED)
, LAST SEQUENCE UPI
, LAST ANNOTATION (
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17; Mismatches 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 102; DB 3; Le
Pred. No. 5.74e-01;
24; Mismatches 62;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PLESSMANN
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LAST
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ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                  POXVIRIDAE;
                                                                                                                                                                                                                                                                                      640
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ALVEOLATA; CILIOPHORA; CILIATA;
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                                  DATA
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                                  BANKS
                                                                                                                                                CHORDOPOXVIRINAE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length
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RESULT 13
ID 059164
AC 059164
AC 059164:
DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
DT 01-NOV-1996 (TREMBLREL. 01, LAST ANONATION UPDATE)
DT 01-NOV-1996 (TREMBLREL. 01, LAST ANONATION UPDATE)
DE SIALIDASE (EC 3.2.1.18) (EXO-ALPHA-SIALIDASE) (NEURAMINIDASE)

MANH.
DE (N-ACYLNEURAMINATE GLYCOHYDROLASE) (ALPHA-NEURAMINIDASE)

ON ACTINOMYCES VISCOSUS.
OS ACTINOMYCES VISCOSUS.
OC PROKARYOTA; FIRMICUTES; IRREGULAR ASPOROGENOUS RODS; CORYNEFORM GR
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN-DSM43798;
RL SUBMITTED (SEP-1991) TO EMBL/GENBANK/DDBJ DATA BANKS.
RR SEQUENCE FROM N.A.
RP SEQUENCE FROM N.A.
RC STRAIN-DSM43798;
RX MEDLINE; 92162190.
RA HEINNINGSEN M., ROGGENTIN P., SCHAUER E.R.;
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Q98187
Q98187;
Q98187;
Q1-FEB-1997
Q1-FEB-1997
Q1-FEB-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SENKEVICH T.G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLLUSCUM CONTAGIOSUM VIRUS VIRUAE; DS-DNA ENVELOPED V. MOLLUSCIPOXVIRUSES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MC018L.
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VIRUS GENES 11:21-29(1995).
EMBL; U34774; G1002997.
EMBL; S82833; G1754760; -.
SEQUENCE 640 AA; 70097 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOSS B.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.
SENKEVICH T.G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   277
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SCIENCE 273:813-816(1996).
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Similarity 36.0%;
27; Conservation
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(TREMBLREL.
(TREMBLREL.
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BUGERT J.J.,
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Pred. No. 5.74e-01;
19; Mismatches 23
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LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDAT
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Pred. No. 5.
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POXVIRIDAE; CHORDOPOXVIRINAE;
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-I- CATALYTIC ACTIVITY: HYDROLYSIS OF 2,3-, 2,6- AND 2,8-GLYCOSIDIC LINKAGES JOINING TERMINAL NON-REDUCING N- OR O-ACYLMEURAMINYL RESIDUES TO GALACTOSE, N-ACETYLHEXOSAMINE, OR N- OR O-ACYLATED NEURAMINYL RESIDUES IN OLIGOSACCHARIDES, GLYCOPROTEINS, GLYCOLIPIDS OR COLOMINIC ACID.

EMBL; X62276; G39255; -.

HYDROLASE; GLYCOSIDASE.
01-FEB-1997
01-FEB-1997
01-JAN-1998
CUT-LIKE 2 (
                                                  P70298;
                                                                                                                                                                                                                                     ANAEROCELLUM THERMOPHILUM.
EUBACTERIA; FIRMICUTES; LOW G+C GRAM-POSITIVE BACTERIA;
CLOSTRIDIACEAE; CELLULOLYTIC THERMOPHILE GROUP; ANAEROCELLUM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                P96311;
P96311;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                  SUBMITTED (MAR-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
-i- FUNCTION: THE N-TERMINAL DOMAIN OF CELA ENCODES FOR AN
-ENDOGLUCANASE ACTIVITY ON CARBOXYMETHYLCELLULOSE. THE C-TERMINAL
DOMAIN PROBABLY ACT SYNERGISTICALLY TO HYDROLYZE CRYSTALLINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01.MAY-1997 (TREMBLREL. 03. CREATED)
01.MAY-1997 (TREMBLREL. 03. LAST SEQUENCE UPDATE)
01.JAN-1998 (TREMBLREL. 05. LAST ANNOTATION UPDATE)
ENDOGLUCANASE A (EC 3.2.1.4) (ENDO-1,4-BETA-GLUCANASE
                                                                                                                                                                                                                                                                                                      (FAMILY 9 OF GLYCOSYL HYDROLASES).
-!- SIMILARITY: THE C-TERMINAL PART BELONGS
(FAMILY 48 OF GLYCOSYL HYDROLASES).
                                                                                                                                                                                                                                                                                                                                                                        CELLULOSE (BY SIMILARITY).
-!- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF 1,4-BETA-D-GLUCOSIDIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN-2-1320;
                                                                                                                                                                                                                                                                                                                                                LINKAGES IN CELLULOSE.
-!- SIMILARITY: THE N-TERMINAL PART BELONGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                816 SPAPSRNAAPTPKPGMEPDEID-RPSDGTMAQPTGAP-ARRVPRRRRRRPAAGCLARDQ 873
                                                                                                                                                                                                                           SEQUENCE
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 (CUX-2)
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larity 34.0%;
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Pred. No. 4.39e-01;
14; Mismatches 31
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Pred. No. 4.39e-01;
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Best Local :
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HOMEOBOX; DNA-BINDING; NUCLEAR PROTEIN.
SEQUENCE 1426 AA; 154703 MW; 478F5;
                                                                                                                                       QUAGGIN S.E., VANDEN HEUVEL G.B., GOLDEN K., BODME
J. BIOL. CHEM. 271:22624-22634(1996).
-!- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
EMBL, U45655; GLS18932; -.
MGD; MGI:107321; CUTL2.
PROSITE; PS00027; HOMEOBOX_1; 1.
                                                                                                                                                                                                                                                      MUS MUSCULUS (MOUSE).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; RODENTIA.
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                    370 LGTEPPYPPQLPPPPGPEDP-LSPSPAQPLLGP-SLGPDGPRNFSL 413
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  LMAEEGVPAPLPPEDAPNAASLAPTPVSPVLEPFNLTSE-PSDYAL 143
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Search completed: Fri Apr 17 13:39:48 1998 Job time: 47 secs.

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	0.4A John F. Collins, Biocomputing Research Unit. (c) 1993-1997 University of Edinburgh, U.K. stribution rights by Oxford Molecular Ltd	Release 3.0.4 Copyright (c) Distr
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Washington University School of Medicine Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286 1800 Fax: 314 286 1810 Email: est@watson.wustl.edu High quality sequence stops: 416	Parsons_J., Rifkin_L., Rollfing_T., Soares_M., Tan,F., Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and Wilson,R. The WashU-Merck EST Project Unpublished (1995)	Eukaryote; Metazoa; Eumetazoa; Bilateria; Coelomata; Eukaryotea; Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes; Barcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Archonta; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 553)	Stowweeks ZNDHP8TOWW VECTOF=97/730 (PHAIMSCLA) WITH a modified polylinker host=DH108 (ampicillin resistant) RSitel=Not I Rsite2=Eco RI two placentae: one from 8 weeks and another from 9 weeks post conception. 1st strand cDNA was primed with a Not I oligo(dT) primer [5'-TGTTACCAATCTGAAGTGGGAGCGGCGCGGATTTTTTTTT	N32077 553 bp mRNA EST 10-JAN-1996 yw97d08.s1 Homo sapiens cDNA clone 260175 3'. N32077 91152476 EST. human clone=260175 primer=m13 -40 forward library=Soares placenta

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EST.
Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Hominidae; 1 (bases 1 to 459).
Hiller,L. Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra, Parsons,J., Rifkin,L., Rohlfing,T., Tan,F., Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and Wilson,R. WashU-Merck EST Project
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Location/Qualifiers
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l Similarity 98.9%;
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IMAGE Consortium (info@image.llnl.gov
Seg primer: ETPrimer
Wigh quality
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WashU-Merck EST Project
Washington University Scho
4444 Forest Park Parkway,
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Fax: 314 286 1810
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/tissue_type="pancreatic islet"
/lab_host="SOLR cells (kanamycin
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  ACTTCGGCGGACCATTANGAATGAGATCCGTGAGATCCTTCCATCTTCTTGAAGTCGCCT
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Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M.,
Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M
Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F.,
Trevaskis, E., Waterston, R., Williamson, A., Wohldmann, P. and
                                                                                                                                                                                                                                                                                                                                                                                                                                456;
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The vector to vector length is 471
Seq primer: -28M13 rev2 from Amersham
High quality sequence stop: 358.
Location/Qualifiers
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WashU-Merck EST Project
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Vertebrata;
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Fax: 314 286 1810
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ilarity 97.9%;
Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="Organ: uterus; Vector: pT7T3-Pac; Site_1: Not I;
Site_2: Eco RI; 1st strand cDNA was primed with a Not I -
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/sex="female"
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/clone="488522"
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Washington University School of Medicine
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Fax: 314 286 1810
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/lab_host="DH10B (ampicillin resistant)"
/complement(<1. .>427)
/db_xref="GDB:6041404"
139 c 78 g 92 t
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487101 3'
AA043722
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WashU-Merck EST Project
WashIngton University School of Medicine
444 Forest Park Parkway, Box 8501, St. I
                                                                                                                                                                                                                                                                    1 (bases 1 to 460)
Hiller,L., Clark,N., Dubuque,T., Elliston,R., Hawkins,M.,
HOlman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
Parsons,J., Rifkin,L., Rohlfing,T., Tan,F., Trevaskis,E.,
Waterston,R., Williamson,A., Wohldmann,P. and Wilson,R.
WashU-Merck EST Project
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EST.
                                                                                                        Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL;
This clone is available royalty-free through LLNL;
IMAGE Consortium (info@image.llnl.gov) for further:
Insert Length: 1290
Sed primer: -40M13 fwd. from Amersham
High quality sequence stop: 381.
Location/Qualifiers
                                                                                                                                                                                     Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                              Unpublished
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Vertebrata;
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pregnant uterus NbHPU
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5′ similar
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g2069789
EST.
Contact: Wilson RK
WashU-Merck EST Project
Washington University S
                                                            1 (bases 1 to 463)
Hiller,L., Allen,M., Bowles,L., Dubuque,T., Gei
Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M.,
Moore,B., Schellenberg,K., Steptoe,M., Tan,F., 7
White,Y., Wylie,T., Watterston,R. and Wilson,R.
Washu-Merck EST project 1997
Unpublished (1997)
                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                  Eukaryotae;
                                                                                                                                                                                                                                human.
                                                                                                                                                                                 Vertebrata; Mammalia;
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complement(<1. .>460)
/db_xref="GDB:3760815"
146 c 83 g
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/db_xref="taxon:9606"
/clone="487101"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /dev_stage="adult"
                                                                                                                                                                                                                                                                                                         463 bp mRNA EST 18-MAY-1997 Soares overry tumor NDHOT Homo sapiens cDNA clone 72390 to SW:GL96_MOUSE P46694 IMMEDIATE EARLY PROTEIN GLY96.
                                                                                                                                                                                  mitochondrial eukaryotes; Metazoa; Chordata; Mammalia; Eutheria; Primates; Catarrhini; Ho
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Pred. No. 0.00e+00;
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M., Martin,J.,
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Local Similarity 97.4%;
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                                                                                                CTACGCTCTGGACCTCAGCACTTTCCTCCAGCAACACCCCGGC 463
                                                                                                                                               GGCGCCCACCCCTGTGTCCCCCCGTCCTCGAGCCCTTTAATCTGACTTCGGAGCCCTCGGA 421
                                                                                   CTACGCTCTGGACCTCAGCACTTTCCTCCAGCAACACCCCGGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -28ml3 rev2 ET from Amersham
High quality sequence stop: 369.
Location/Qualifiers
W52268 447 bp mRNA EST 11-OCT-1996 ZC46a10.r1 Soares senescent fibroblasts NbH5F Homo saptens CDNA clone 325338 5' similar to SW:GL96_MOUSE P46694 IMMEDIATE EARLY PROTEIN GLY96. [1] ;.
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/lab_host="DH10B (ampicillin resistant)"
<1. .>463
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/clone="723904"
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196 c 114 g
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone_lib="Soares ovary
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Pred. No. 0.00e+00;
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Query Match 33.1%;
Best Local Similarity 96.7%;
Matches 433; Conservative
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                                                   TCCCGGGACCCCGGGGGCTCCGGTCCTGAGATCTTCACCTTCGACCTCTCCCGGAGC
                                                                                                                                        CCGCAGCGGACCCATGCCGGGCGCCCCAGCNTCATCNGCGGGCACCGAAAGCGCAGCAGC
AAAAGGCTTCTCTTTCTGCTGCTCACCATCGTCTTCTGCCAGATCCTGATGGCTGAAGAG
              AAAAGGCTTCTCTTCTGCTGCTCACCATCGTCTTCTGCCAGATCCTGATGGCTGAAGAG
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g1349380
EST.
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Fax: 314 286 1810
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4444 Forest Park Parkway,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Wilson RK
WashU-Merck EST Project
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Unpublished (1995)
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/tissue_type="senescent fibroblast"
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Pred. No. 0.00e+00;
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Le, M., Lennon, G., Marra, M.,
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4444 Forest Park Parkway, Box 8501, St. I
                                                                                                                                                                                                                                                                                                                                                                                                                                              IMAGE Consortium (info@image.linl.gov) for Insert Length: 1245 Std Error: 0.00 Seq primer: -40M13 fwd. from Amersham High quality sequence stop: 420.
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WashU-Merck EST Project
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EST.
                                                                                                                                                                         human clone-259649 primer-ml3 -40 forward library-Soares placenta 8to9weeks 2NbHP8to9w vector-P7713D (Pharmacia) with a modified polylinker host-DH10B (ampicillin resistant) Rsitel-Not I Rsite2-Eco RI two placentae: one from 8 weeks and another from 9
                                                                                                                                                                                                                                                                                                                                                                                                                                              yw91h09.sl Homo sapiens cDNA clone 259649 3.
                                                                          Deuterostomia; Chordata; Vertebrata; Gnathostomata; Os:
Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia;
Eutheria; Archonta; Primates; Catarrhini; Hominidae; H
                                                                                                                                                          Homo sapiens
                                                                                                                                         Eukaryotae; Metazoa; Eumetazoa; Bilateria;
                   Holman, M., Hultman, M.,
(bases 1 to 390)
(bases 1 to 390)
(tases 1 to 390)
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/tissue_type="senescent fibroblast"
/lab_host="DH10B (ampicillin resistant)"
complement(<1. .>413)
a 136 c 77 g 89 t 1 others
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/clone="325338"
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Pred. No. 0.00e+00;
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                   Le,M.,
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Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo
1 (bases 1 to 443)
1 (bases 1 to 443)
1 Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra, I
Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
                                                                                                                                                                              W47587 443 bp mRNA EST 11-OCT-1996 ZG35b02r1 Soares senescent fibroblasts NbHSF Homo sapiens CDNA clone 324267 5' similar to SW:GL96_MOUSE P46694 IMMEDIATE EARLY PROTEIN GLY96. [1] ;.
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Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
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Fax: 314 286 1810
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/clone="259649"
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Pred. No. 0.00e+00;
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                         GGACT 442
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This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 1411 *Std Error: 0.00
Seq.primer: mob.REGA+ET
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WashIngton University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
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Fax: 314 286 1810
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Location/Qualifiers
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/tissue_type="senescent fibroblast"
/lab_host="DH10B (ampicillin resistant)"
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                                               AAGATGGAAGGATCTCACGGATCTCATTCCTAATGGTCCGCCGAAGTCTCACACAGTAGA 183
                                                                                                                  CGTGACAGCCCAACCAACCCCAACCCTCTACCTCGCAGCCACCCTAAAAGGNGACTTCAAG 123
CAGACGGAGTTGAGATGCTGGAGGATGCAGTCACCTCCTAAACTTACGACCCACCACCAG
                                                                                                                                                                   GACAGTAAATCAATTTTATTTGTGTTCACAGAACATACTAGGCGATCTCGACAGTCGCTC 1145
                                                                                                  CGTGACAGCCCACCCCAACCCCCAACCCTCTACCTCGCAGCCACCCTAAAGGCGACTTCAAG
                                 AAGATGGAAGGATCTCACGGATCTCATTCCTAATGGTCCGCCGAAGTCTCACACAGTAGA 1025
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WashU-Merck EST Project
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Unpublished (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryòtae; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Euteria; Primates; Catarrhini; Hominidae; R(1 (bases 1 to 375)

1 (bases 1 to 375)

Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M. Holman,M., Kucaba,T., Le,M., Lennon,G., Marz, Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. (
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                 /db_xref="taxon:9606"
/clone="324267"
/clone=lib="Soares senescent fibroblasts_NbHSF"
/tissue_type="senescent fibroblast"
/lab_host="DH10B (ampicillin resistant)"
complement(<1. .>375)
125 c 70 g 80 t 1 others
                                                                                                                                                                                                                                   Score 368; DB 15;
Pred. No. 0.00e+00;
0; Mismatches 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                School of Medicine way, Box 8501, St.
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Le,M., Lennon,G., Marra,
., Soares,M., Tan,F.,
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                                                                                                                                                                                                                                                                   Length 375;
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488522 3'.
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Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M. Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevaskis, E., Waterston, R., Williamson, A., Wohldmann, P. and
                                Similarity
351; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                 This clone is available royalty-free through LLNL; MAGE Consortium (info@image.llnl.gov) for further i Seq primer: -40M13 fwd. from Amersham High quality sequence stop: 324.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Wilson RK
WashU-Merck EST Project
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         numan
                                                                                                                 91
                                                                                                                                                                                                              double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the No and Eco RI sites of the modified pT7T3 vector. Library went through one round of normalization. Library constructed by M. Fatima Bonaldo."

/db_xref-"taxon:9606"
                                                                                                                                                                                                                                                                                                                                                Site_2: Eco RI; 1st strand oligo(dT) primer [5'
                                                                                                                 complement(<1. .: 121 c 66
                                                                                                                                                                                                                                                                                                                                   /note="Organ: uterus; Vector: pT7T3-Pac; Site_1: Site 2: Eco RI; 1st strand cDNA was primed with a
                                                                                                                                              /dev_stage="adult"
/lab_host="DH10B"
                                                                                                                                                                                  /sex-"
                                                                                                                                                                                                /clone_lib="Soares pregnant uterus NbHPU"
                                                                                                                                                                                                                                                                                                                                                                                               'organism="Homo sapiens"
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 1184 TGTGTTCACAGAACATACTAGGCGATCTCGACAGTCGCTCCGTGACAGCCCACCAACCCC 1125
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                   ACTTCATCCCAGCCGGGACGTCCTCCCCCACCCGAGTCCTCCCCATTTCTTCTTCTACTT
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4444 Forest Park Parkway,
Tel: 314 286 1800
Fax: 314 286 1810
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Unpublished (1995)
Other_ESTs: ya76f12.rl
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eucaryotae; Metazoa; Chordata; Vertebrata; Gnathostomata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 405)
Hillier,L., Clark,N., Dubbque,T., Elliston,K., Hawkins,M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             human clone=67631 library-Stratagene placenta (#937225)
vector-pBluescript SK- host-SOLR cells (kanamycin resistant)
primer:-21m13 Rsitel-Ecorl Rsite2-Xhor Placental tissue from a
Caucasian male. Cloned unidirectionally, Primer: Oligo dT. Average
insert size: 1.2 kb; Uni-ZAP XR Vector; 5' adaptor sequence:
5'-GANITCGCACGAG-3', 3', adaptor sequence:
5'-CTCGAGTTTTTTTTTTTTTTTTTTTT-3'.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g651392
                                                                                                                                                                                                                                  Email: est@watson.wustl.edu
Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL;
IMAGE Consortium (info@image.llnl.gov) for further i
                                                                                                                                                                                                                                                                                                                                                                       Contact: Wilson RK
WashU-Merck EST Project
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                                                                    Conservative
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                                                                                                                                                   /organism="Homo sapiens"
/clone="67631"
1 132 c 81 g 8
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sapiens
                                                                Score 345; DB 9;
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ACCESSION
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Bult, C.J., Lee, N.H., Kirkness, E.F., Weinstock, K.G., Gocayne, J.D.,
White, O., Sutton, G., Blake, J.A., Brandon, R.C., Man-Wai, C.,
Clayton, R.A., Cline, T.R., Cotton, M.D., Earle-Hughes, J., Fine, L.D.,
Fitzgerald, L.M., Fitzhugh, W.M., Fritchman, J.L., Geoghagen, N.S.,
Glodek, A., Gnehm, C.L., Hanna, M.C., Hedblom, E., Hinkle, P.S., Or.,
Kelley, J.M., Kelley, J.C., Liu, L.-I., Marmaros, S.M., Merrick, J.M.,
Moreno-Palanques, R.F., McDonald, L.A., Nguyen, D.T., Pelligrino, S.M.,
Phillips, C.A., Ryder, S.E., Scott, J.L., Saudek, D.M., Shirley, R.,
Small, K.V., Spriggs, T.A., Utterback, T.R., Weidman, J.F., Li, Y.,
Bednarik, D.P., Cao, L., Cepeda, M.A., Coleman, T.A., Collins, E.J.,
Dinke, D., Feng, D.-F., Ferrie, A., Fischer, C., Hastings, G.A.,
He, W.W., Hu, J.S., Greene, J.M., Gruber, J., Hudson, P., Kim, A.K.,
Kozak, D.L., Kunsch, C., Hungjun, J., Li, H., Meissner, P.S., Olsen, H.,
Raymond, L., Wei, Y.F., Wing, J., Xu, C., Yu, G.L., Ruben, S.M.,
Dillion, P.J., Fannon, M.R., Rosen, C.A., Haseltine, W.A., Fields, C.,
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AA301628
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Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of cDNA sequence
Nature 377 (6547 Suppl), 3-174 (1995)
96026280
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Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
                                                          Email: arkerlav@tigr.org
For clone availability, additional sequence and expression
information related to this EST, please check the TIGR Human Gene
Index (http://www.tigr.org/tdb/hgi/hgi.html)
Seq primer: M13 Reverse.
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/organism="Homo sapiens"
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                  ACGTAATATTTTATTT
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                                                         CTCCT-AATTAAT-ATTTATATGTATTTATGTACGTCCTCCTA-GGTGATGGAGATGTGT
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                                                                                                                  CAGCCCAGCTGGGG-CTAGGCCCGGTGGGAAGGAGCGTCGTTAATTTATTTCTTATTG
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ECORI; Site_2: XhoI"
/db_xref="hATCC (inhost):113941"
/db_xref="taxon:9606"
/clone_lib="hAorta endothelial cells"
/cell_type="endothelial cell"
/dev_stage="adult"
                                                                                                                                                                                                                                                                                                                                                                                                                           27.0%;
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   798
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Pred. No. 0.00e+00;
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                                                                                                                                                                                                                                                                                                                                                                                                                  RA SCHBILL D.A., JOHNSTON G.I., PAGE S.O., MOSLEY M.J., WILSON K.H.,
RA WORMAN N.P., CAMPBELL S., FIDOCK M.D., FURNESS L.M.,
RA PARRY-SMITH D.J., PETER B., BAILEY D.S.;
RA PARRY-SMITH D.J., PETER B., BAILEY D.S.;
RI J. PHARMACOL EXP. THER. 272:134-142(1995).
C. -!- FUNCTION: THIS ALPHA-ADRENERGIC RECEPTOR MEDIATES ITS ACTION BY
C. --- SUSCILATION WITH G PROTEIN ACTIVATE A PHOSPHATIDYLINOSITOL-
C. --- CALCIUM SECOND MESSENGER SYSTEM
C. --- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
C. --- SUBLIARITY: BELONGS TOF FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
EMBL: M99599; --- NOT_ANNOTATED_CDS.
EMBL: M99599; --- NOT_ANNOTATED_CDS.
EMBL: L11773; G666891; --.
DR EMBL: L11773; G666891; --.
DR GCROB; GCR_0530; --.
DR GCROB; GCR_0530; --.
DR MTW. 104270. ---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE; 94239386.
FORRAY C., BARD J.A., WETZEL J.M., CHIU G., SHAPIRO E., LEPOR H., HARTIG P.R., WEINSHANK R.L., BRANCHEK T.A., GLUCHOWSKI C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE: 93016158.
RAMARAO C.S., DENKER J.M.,
GRAHAM R.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HOMO SAPIENS (HUMAN).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
                                                                                                                                                                                                                                                                                                                            PROSITE; PS00237;
G-PROTEIN COUPLED
MULTIGENE FAMILY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. MEDLINE; 95114877.
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EUTHERIA; PRIMATES
                                                                                                                                                                                                                                                                                                          DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOL. PHARMACOL. 45:703-708(1994).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BIOL. CHEM. 267:21936-21945(1992).
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Similarity 28.6%;
18; Conservative
       G_PROTEIN_RECEPTOR; 1.
RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN;
PHOSPHORYLATION; LIPOPROTEIN; PALMITATE.
45
EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PEREZ D.M.,
1 (POTENTIAL).

CYTOPLASMIC (POTENTIAL).

2 (POTENTIAL).

EXTRACELLULAR (POTENTIAL).

3 (POTENTIAL).

CYTOPLASMIC (POTENTIAL).

4 (POTENTIAL).

5 (POTENTIAL).

5 (POTENTIAL).

CYTOPLASMIC (POTENTIAL).

6 (POTENTIAL).

EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 98; DB 1; Length 475;
Pred. No. 6.05e-01;
19; Mismatches 24; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GAIVIN R.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RIEK R.P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TANG
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             В
                                                       Matches
                                 Query Match
Best Local
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CARBOHYD
DISULFID
LIPID
CONFLICT
CONFLICT
CONFLICT
CONFLICT
                                                                                                                          TRANSMEM
DOMAIN
DOMAIN
                                                                                                             CARBOHYD
                                                                                                                     CARBOHYD
       12 TILQAPTPAPSTIPGPRRGSGPEIFTFDPLPEPAAAPAGRPSASRG
                          h 8.8%;
Similarity 41.3%;
19; Conservative
                                                       A.
                                                       340
379
379
10
24
29
29
34
195
365
370
50778
                                                       MW;
                                                    POTENTIAL.

POTENTIAL.

POTENTIAL.

POTENTIAL.

BY SIMILARITY.

BY SIMILARITY.

PALMITATE (POTENTIAL).

MISSING (IN REF. 1).

MASAD -> PRH (IN REF. 1).

R -> RG (IN REF. 2).

MW; D088058C CRC32;
                          Score 98; DB 1; Length 519; Pred. No. 6.05e-01; 9; Mismatches 15. Todal-
                                                                                                                          7 (POTENTIAL).
CYTOPLASMIC (POPOLY-ARG.
 57
                            ω
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                            Gaps
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Search completed: Fri Apr 17 13:38:42 1998 Job time : 10 secs.

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RESULT
OCCUPANT
OCCUP
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RESULT 13
ID VGLI_HSV11
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                                                                                                                                                                                                                                                                    Query Match 8.8%;
Best Local Similarity 36.7%;
Matches 22; Conservative
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                               -1- SIMILANIA...

EMBL; X65265; G42201; -.

PIR; S28013; S28013;

PROSITE; PS01141; T2SP_C; 1.

TPANSPORT; TRANSMEMBRANE; INNER MEMBRANE.

CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GSQC_ERWCH STANDARD: PRT; 272 AA. 001564; 01-JUL-1993 (REL. 26, CREATED) 01-JUL-1993 (REL. 26, LAST SEQUENCE UPDATE) 01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE) 01-NOV-1995 (REL 32, LAST ANNOTATION UPDATE) 01-NOV-1995 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LINDEBERG M., COLLMER A.;

J. BACTERIOL. 174:7385-7397(1992).

-i- FUNCTION: INVOLVED IN A GENERAL SECRETION PATHWAY (GSP)
EXPORT OF PROTEINS. REQUIRED FOR THE TRANSLOCATION OF THE MULTIPLE PECTIC ENZYMES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ERWINIA CHRYSANTHEMI. PROKARYOTA; GRACILICUTES;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OUTC).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -!- SUBCELLULAR LOCATION: INNER MEMBRANE (PROBABLE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE; 93054355
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                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                     DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     75 LPVEEPNPAKRLLFLLTIVFCQILMAEEGVPAPLPPEDAPNAASLAPTPVSPVLEPFNL 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local
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ITE; PS01141; T
                                                                                                                                     LPVEEPNPAKRLLFLLLTIVFCQILMAEEGVPAPLPPEDAPNAASLAPTPVSPVLEPFNL
                                                                                                                                                                                               LPPLSPSVIRRILFYLLMLLFCQQL-AMIFWRIGLP-DNAP-VSSVQITPAQARQQPVTL
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22; Conser
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36
272 AA;
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36
272 AA;
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TRANSMEMBRANE; INNER MEMBRANE.
1 16 CYTOPLASMIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
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35
272
30162
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36.78;
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272
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                                                                                                                                                                                                                                                                                                                                                                                                      MW;
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                                                                                                                                                                                                                                                                    Score 98; DB 1; Leg
Pred. No. 6.05e-01;
11; Mismatches 24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11;
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Pred. No. 4.56e-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    POTENTIAL.
PERIPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                      PERIPLASMIC (POTENTIAL)
25634B57 CRC32;
             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7944F46D CRC32;
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             390
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Best Local Similarity
Matches 25; Conse
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01-JAN-1988 (
01-JAN-1988 (
01-OCT-1996 (
GLYCOPROTEIN
NP_BIND
ACT_SITE
ACT_SITE
SEQUENCE
                                                                                                 STRAIN-NGS SEROTYPE C;

MEDLINE; 95270576

BOYD D.A., CVITKOVITCH D.G., HAMILTON I.R
J. BACTERIOL. 177:2622-2627(1995).

-i- FUNCTION: IMPORTANT AS A MEANS OF GEN
BIOSYNTHETIC REACTIONS.

-i- CATALYTIC ACTIVITY: D-GLYCERALDEHYDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CARBOHYD
CARBOHYD
                                                   PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; L00036; G291497; -. EMBL; X14112; G59565; -. EMBL; X02138; G59879; -.
                              OXIDOREDUCTASE;
NP_BIND 230
                                                                                                                                                                                             STREPTOCOCCUS MUTANS. PROKARYOTA; FIRMICUTES;
                                                                                                                                                                                                                                              NADP-DEPENDENT GLYCERALDEHYDE-3-PHOSPHATE DEHYDROGENASE (EC 1.2.1.9) (NON-PHOSPHORYLATING GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE)
                                                                                                                                                                                                                                                                   01-NOV-1997
01-NOV-1997
                                                                                                                                                                                                                                                                                       Q59931;
01-NOV-1997
                                                                                                                                                                                                                                                                                                          GAPN_STRMU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GG, GD, GI, AND GE.
-!- SIMILARITY: TO OTHER HERPESVIRUSES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MCGEOCH D.J., DOLAN A., DONALD J. MOL. BIOL. 181:1-13(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HERPES SIMPLEX VIRUS (TYPE VIRIDAE; DS-DNA ENVELOPED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GI OR US7
                                                                        EMBL;
                                                                                -!- SIMILARITY: BELONGS TO THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GLYCOPROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. MEDLINE; 85160822.
                                                                                                                                                                           SEQUENCE FROM N.A
                                                                                                                                                                                                                            DEHYDROGENASE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CARBOHYD
                                                                                                                                                                                                                                     GLYCERALDEHYDE-3-PHOSPHATE DEHYDROGENASE (NADP+))
                                                                                                                                                                                                                                                                                                                                                                       264
                                                                                                                                                                                                                                                                                                                                                                                                            206 QASTPSTTTSTPSTTIPAPSTTIPAPQASTTP-FPTGDPKPQPPGVNHEPPSNA-TRATR 263
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                                                                                                                                                                                                                                                                                                                                                                      DSR--YALTVTQIIQIAIPASIIALVFL
                                                                                                                                                                                                                                                                                                                                                                                           HSRSCHPTMTILQAPTPAPST-IPGPRRGSGPEIFTFDPLPEPAAAPAGRPSASRGHRKR
                                                                       L38521;
                                                                                           3-PHOSPHO-D-GLYCERATE +
                                                 PS00070; ALDEHYDE_DEHYDR_CYS; PS00687; ALDEHYDE_DEHYDR_GLU;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        156
175
257
390 AA;
                                                                                                                                                                                                                                                                  (REL.
  475
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                       G642667;
  ξ
                             NADP.
235
                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                  35, CREATED)
35, LAST SEQUENCE UPDATE)
35, LAST ANNOTATION UPDATE)
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175
257
41369
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (TYPE 1 / STRAIN 17).
LOPED VIRUSES; HERPESVIRIDAE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CREATED)
LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
                                                                                                                                                                                               COCCI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MW;
   Ĭ.
          NAD (ADP PART)
BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                Score 98; DB 1;
Pred. No. 6.05e-
21; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  POTENTIAL.
POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GLYCOPROTEINS IN HSV1
                                                                                            NADPH
                                                                                                                                                                                                                                                                                                           PRT;
                                                                                ALDEHYDE
                                                                                                                                                                                               STREPTOCOCCAEAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    S., RIXON F.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7DA38E2D CRC32;
                                                                                                                                                                                                                                                                                                                                                   89
                                                                                                                                                                                                                                                                                                                                                                      289
                                                                                                                                                                                                                                                                                                           475
                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 1;
6.05e-01
                                                                                                                        GENERATING NADPH FOR
                                                                                                                                           I.R.;
                                                 1.
FALSE_NEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GLYCOPROTEINS
                                                                                DEHYDROGENASES
                                                                                                   3-PHOSPHATE + NADP(+)
                                                                                                                                                                                                                                                                                                           3
                              (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                   37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ALPHAHERPESVIRINAE
                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AND
                                                                                                                                                                                                                                 (TRIOSEPHOSPHATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'n
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ..
..
                                                                                FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GB,
                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local S
Matches 2
                                                                                  PIR: E30341; E30341
GCRDB; GCR_D017; --
PROSITE; PS00237; C
G-PROTEIN COUPLED I
MULTIGENE FAMILY; E
NON_TER
TRANSMEM <1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AGEYAMA R. SASAI Y., NAKANISHI S.;

J. BIOL. CHEM. 266:15525-15531(1991)
-I - FUNCTION: C/EBP IS A DNA-BINDING PROTEIN THAT RECOGNIZES '
DIFFERENT MOTIFS: THE CCAAT HOMOLOGY COMMON TO MANY PROMO
THE ENHANCED CORE HOMOLOGY COMMON TO MANY ENHANCERS.
-I SUBUNIT: BINDS DNA AS A DIMER.
-I SUBCELLULAR LOCATION: NUCLEAR.
-I TISSUE SPECIFICITY: UBIODITOUSLY EXPRESSED.
-I SINILARIY: TO OTHER BZIP PROTEINS. STRONG, TO OTHER C/EB
            TRANSMEM
DOMAIN
TRANSMEM
                                               DOMAIN
TRANSMEM
DOMAIN
                                                                                                                                                                       EMBL;
                                                                                                                                                                                 LIBERT F., PARMENTIER M., LEFORT A., DINSART C., VAN SANDE MAENHAUT C., SIMONS M.-J., DUMONT J.E., VASSART G.;
SCIENCE 244:569-572(1989).

-!- FUNCTION: THIS ALPHA-ADRENERGIC RECEPTOR MEDIATES ITS A ASSOCIATION WITH G PROTEINS THAT ACTIVATE A PHOSPHATIDY CALCIUM SECOND MESSENGER SYSTEM.

-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.

-!- SUBCELLULAR ECCANTION: INTEGRAL MEMBRANE PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                     Alab_Canfa STANDARD; PRT; 417 AA. P1615; 01-OCT-1989 (REL. 12, CREATED) 01-FEB-1996 (REL. 12, LAST SEQUENCE UPDATE) 01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE) ALPHA-1B ADRAIB OR REC5.
                                                                                                                                                                                                                                                                                      MEDLINE; 89242119
                                                                                                                                                                                                                                                                                                   TISSUE-THYROID;
                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                  CANIS FAMILIARIS (DOG).
EUKARYOTA; METAZOA; CHORDATA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; M65149; G203412; PIR; B39429; B39429. TRANSFAC; T00109; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CEBPD OR CELF.
RATTUS NORVEGICUS (
EUKARYOTA; METAZOA;
                                                                                                                                                                                                                                                                                                                                         EUTHERIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TRANSCRIPTION REGULATION; ACTIONA_BIND 197 215 1
DOMAIN 226. 254
SEQUENCE 268 AA; 28600 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EUTHERIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           142 CAQTVVSLAAAAQPTPPTSPEPPRGSPGPSLAP-GPVREKGAGKRGPDRGSPEYRQRRER 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity 36.7%; nes 22; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  X14050;
                                                                                                                                                                                                                                                                                                                                         CARNIVORA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RODENTIA.
  45
45
65
105
                                                                                                                                                            E30341.
                                                                                                                                                                         G833784;
                                                                                                           G_PROTEIN_RECEPTOR; 1.
RECEPTOR; TRANSMEMBRANE; GLYC PHOSPHORYLATION; LIPOPROTEIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (RAT)
  8
20
44
64
85
104
127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ACTIVATOR; DNA-BINDING;
BASIC MOTIF.
EXTRACELLULAR (POTENTIAL).
3 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
4 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
5 (POTENTIAL).
5 (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 101; DB 1;
Pred. No. 2.57e-01;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LEUCINE-ZIPPER.
; 760E79C0 CRC32;
                                                                                                                                                                                                                                                                                                                                                  VERTEBRATA;
                                                                                     (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                     G-PROTEIN COUPLED RECEPTORS
                                                                                                                                                                                                                                                                                                                                                   TETRAPODA;
                                                                                                                        GLYCOPROTEIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length
                                                                                                                                                                                                                        DIATES ITS ACTION BY PHOSPHATIDYLINOSITOL-
                                                                                                              PALMITATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUCLEAR
                                                                                                                                                                                                                                                                                                                                                   MAMMALIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROMOTERS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C/EBF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROTEIN
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Best Local S
Matches 1
                                                                                                                                                                                         Query Match
Best Local S
Matches
                                                                                                                                                                                                             PIR: F344/,
TRANSFAC; T00709;
PROSITE; PS00463; ZN2_CY6_FUNGAL_1; 1.
PROSITE; PS50048; ZN2_CY6_FUNGAL_2; 1.
TRANSCRIPTION REGULATION; ACTIVATOR; DNA-BINDING; NUCLEAR ;
ZINC; METAL-BINDING; QUINATE METABOLISM.
DNA_BIND 76 103 ZN(2)-CYS(6), FUNGAL-TYPE. M.
DOMAIN 773 793 ASP/GLU-RICH (ACIDIC).
DOMAIN 773 793 ASP/GLU-RICH (ACIDIC).
TOTHER 816 AA; 88946 MW; E99EACA7 CRC32;
                                        01-JUL-1993 (REL. 2
01-JUL-1993 (REL. 2
01-NOV-1995 (REL. 3
GENERAL SECRETION I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-OCT-1989
01-OCT-1989
01-AUG-1992
                               GENERAL OUTC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TRANSMEM
DOMAIN
TRANSMEM
DOMAIN
DOMAIN
DOMAIN
DISULFID
LIPID
                                                                                      GSPC_ERWCH
P31698;
                                                                                                                                                                                                                                                                                                                                                                        MEDLINE; 89293848.

GEEVER R. F., HULET L., BAUM J.A., TYLER B.M., PATEL V.B.,

RUTLEDGE B.J., CASE M.E., GILES N.H.;

J. MOL. BIOL. 207:15-34 (1989).

-!- FUNCTION: TRANSCRIPTION ACTIVATION OF GENES FOR ENZYMES AND
PROTEINS OF QUINATE METABOLLSM BY BINDLING TO A 16 BASE-PAIR
SEQUENCE (CONSENSUS GERTAARKETTAYCC) IN FRONT OF EACH QA GE
-!- SUBCELLULAR LOCATION: NUCLEAR.
-!- SIMILARITY: CONTAINS A ZN(2)-CYS(6), FUNGAL-TYPE BINUCLEAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QA1F_NEUCR
P11638;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NEUROSPORA CRASSA.
EUKARYOTA; FUNGI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QUINIC ACID QA-1F.
ERWINIA CHRYSANTHEMI. PROKARYOTA; GRACILICUTES;
                                                                                                                                                                                                                                                                                                                            CLUSTER DOMAIN.
EMBL; X14603; G3068; -.
PIR; S04256; S04256.
PIR; F31277; F31277.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
STRAIN-74-OR23-1A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                    408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 353 ALLSLPAPQPPGRRG-RRDSGP-LFTFRLLAERGSPAAG
                                                                                                                                               70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12 TILQAPTPAPSTIPGPRRGSGPEIFTFDPLPEPAAAPAG
                                                                                                                                            VVRTQLPPDDDRPRPRMRALLVACEIVDTIVSMRHNVPAHLKPDDIAD 455
||| ||| :: | :: :: ||| | :| :: |
| VRRQLPVEEPNPAKRLLFLLTIVFCQILMA-EEGVPAPLPPEDAPN 116
                                                                                                                                                                                         h 9.1%;
Similarity 33.3%;
16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           268
417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (REL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 UTILIZATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    199
223
230
244
271
271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8
                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      222
229
243
417
281
281
98
268
45891
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12, CREATED)
12, LAST SEQ
23, LAST ANN
                                          26, CREATED)
26, LAST SEQUENCE UPDATE)
32, LAST ANNOTATION UPDAT
PATHWAY PROTEIN C (PECTIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ASCOMYCOTINA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
ON ACTIVATOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WW.
SCOTOBACTERIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6 (POTENTIAL).

EXTRACELLULAR (POTENTIAL).
7 (POTENTIAL).
CYTOPLASMIC (POTENTIAL POLY-ARG.
BY SIMILARITY.
PALMITATE (POTENTIAL).
PALMITATE (POTENTIAL).
                                                                                                                                                                                        Score 101; DB 1;
Pred. No. 2.57e-01;
13; Mismatches 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score
Pred.
                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PYRENOMYCETES;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            101; DB 1;
No. 2.57e-01;
                                         ON UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         816
                                                                                                   272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (POTENTIAL).
 FACULTATIVELY
                                                                                                  ΑA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (POTENTIAL).
                                           ENZYMES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          389
                                                                                                                                                                                           18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SORDARIALES
                                                                                                                                                                                          Indels
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                                           SECRETION
 ANAEROBIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2
                                                                                                                                                                                                                                                                                                                                                                                                  GENE
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 RODS;
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RESULT
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Best Local Similarity 23.7%;
Matches 31; Conservative
                                                                                                                                                                                           WILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M.,
BONFIELD J., BURTON J., CONNELL M., COPSEY T., COOPER J., COULSON A.,
CRAXTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FRASER A.,
FULTON L., GARDNER A., GREEN P., HAWKINS T., HILLIER L., JIER M.,
JOHNSTON L., JONES M., KERSHAW J., KIRSTEN J., LAISSTER N.,
LATREILLE P., LICHTNING J., LLOYD C., MORTIMORE B., O'CALLAGHAN M.,
PARSONS J., PERCY C., RIFKEN L., ROOPRA A., MONDERS D., SHOWNKEEN R.,
SIMS M., SWALDON N., SMITH A., SMITH M., SONNHAMMER E., STADEN R.,
SULSTON J., THIERRY-MIEG J., THOMAS K., VAUDIN M., VAUGHAN K.,
WATERSON R., WATSON A., WEINSTOCK L., WILKINSON-SPROAT J.,
CHILLIAND R., WATSON A., WEINSTOCK L., WILKINSON-SPROAT J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-JUN-1994 (REL. 29, CREATED)
01-JUN-1994 (REL. 29, LAST SEQUENCE UPDATE)
01-FEB-1995 (REL. 31, LAST ANNOTATION UPDATE)
FORMIN 4 (LIMB DEFORMITY PROTEIN).
                                                                                                                                                                                                                                                                                                                                                                                                                         MUS MUSCULUS (MOUSE).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; RODENTIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NATURE 368:32-38(1994).
EMBL; L16621; G289783; -.
PIR; S44920; S44920.
EMBL; X62379; G51553; -.
PIR; S24407; S24407.
HSSP; P19999; ICLG.
NUCLEAR PROTEIN; DEVELOPMENTAL PROTEIN; ALTERNATIVE DOMAIN 635 638 POLY-SER.
DOMAIN 644 744 PRO-RICH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FOR4_MOUSE Q05859;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WORMPEP: 2K688.5; CE00463.
PROSITE; PS50053; UBIQUITIN_2; UNKNOWN_1.
HYPOTHETICAL PROTEIN.
SEQUENCE 1799 AA; 202641 MW; 3EF7DDB2
                                                                                                                                                                                                                                                                                                                                                                           TISSUE-EMBRYO;
                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WOHLDMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       962 FEFDLSGSSDQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      844 FLENRGRIPSTSSAPSTSENPPGPSFNS-EDAADIRAGRLPLGTRPNRRTVRETVHPAAA 902
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       72 RR-QLPVEEPNPAKRLLFLLLTIVFCQILMAEEGVPAPLP-PEDAPNAASLAPTPVSPVL 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13 ILQAPTPAPSTIPGPRRGSGPEIFTFDPLPEPAAAPAGR-PSASRGHRKRSRRVLYPRVV 71
                                                                                                LIMB BUD.

ALTERNATIVE PRODUCTS: MANY DIFFERENT FORMS OF THIS PROTEIN ARE PRODUCED BY ALTERNATIVE SPLICING OF THE LD GENE. A VARIATION IN SPLICING IS SEEN AMONG DIFFERENT TISSUES AND DIFFERENT SIZE TRANSCRIPTS EXIST WITHIN ANY ONE TISSUE. THIS: IS ISOFORM 4 AND DIFFERENT IN ITS N-TERMINAL TO THE OTHER MOUSE ISOFORMS SO FAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EPFNLTSEPSD 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ARAESPNHISLTFTATTHTFAPAGF-PLMMASSNVPSTSAGPPGWPIRQVVSPTPTTRGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         972
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 109; DB 1; Le
Pred. No. 2.43e-02;
30; Mismatches 65;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3EF7DDB2 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          B
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                                 SPLICING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5
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AND MAY HAVE A FUNCTION IN DIFFERENTIATED CELLS OR MAY BE
INVOLVED IN MAINTAINING SPECIFIC DIFFERENTIATED STATES.

C:- SUBCELLULAR LOCATION: NUCLEAR.

C:- I- TISSUE SPECIFICITY: IT IS PRESENT IN THE ADULT KIDNEY, TESTIS,

C:- I- TISSUE SPECIFICITY: IT IS PRESENT IN THE ADULT KIDNEY, TESTIS,

C:- I- TISSUE SPECIFICITY: IT IS PRESENT IN THE ADULT KIDNEY, TESTIS,

C:- I- LIMB, OVARY, BRAIN, SMALL INTESTINE, SALIVARY GLAND AND HARDERIAN

C:- GLAND. IT IS PRESENT THROUGHOUT THE EMBRYO.

C:- I- DEVELOPMENTAL STAGE: IN THE DEVELOPING LIMB BUD, THE PROTEIN

C:- I- DEVELOPMENTAL STAGE: IN THE DEVELOPING LIMB BUD, THE PROTEIN

C:- I- DEVELOPMENTAL STAGE: IN THE DEVELOPING LIMB BUD, THE PROTEIN

C:- COMPARTMENT, PREDOMINANTLY IN THE POSTERIOR REGION. DURING

KIDNEY MORPHOGENESIS, EXPRESSION IS INITIALLY RESTRICTED TO

C:- ALTERNATIVE PRODUCTS: MANY DIFFERENT FORMS OF THIS PROTEIN

C:- ALTERNATIVE PRODUCTS: MANY DIFFERENT FORMS OF THIS PROTEIN

C:- ALTERNATIVE PRODUCTS: MANY DIFFERENT TISSUES AND

C:- ALTERNATIVE SPLICING OF THE LD GENE. A

VARIATION IN SPLICING IS SEEN AMONG DIFFERENT TISSUES AND

C:- ALTERNATIVE SPLICING OF THE LD GENE. A

VARIATION IN SPLICING IS SEEN AMONG DIFFERENT TISSUES AND

C:- EMBL; X33599; G52878; -.

DR HASSP; P19999; ICLG.

DR HASSP; P19999; ICLG.

DR HASSP; P19999; ICLG.
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Best Local
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Best Local
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01-JUN-1994 (REL. 2
01-JUN-1994 (REL. 2
01-NOV-1997 (REL. 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DOMAIN
SEQUENCE
                                             LT 8
CEBD R1
STANDARD; PRT; 268 AA.
Q03484;
01-OCT-1996 (REL. 34, CREATED)
01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)
01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DOMAIN
DOMAIN
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FACTOR CELF).
                            CCAAT/ENHANCER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MGD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MUS MUSCULUS (MOUSE).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FMN OR LD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EUTHERIA; RODENTIA.
                                                                                                                                                                                                                                                                                                  942 VLALPNSGGPPP-PPPPPPPPPPPGLAPPPP-PPGL-SFGLSSSSSQYP 984
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         716 VLALPNSGGPPP-PPPPPPPPPPPPPPPPPPPPPPPPPPPPP-PPGL-SFGLSSSSSQYP 758
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  86
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                                                                                                                                                                                                                                                                      98 IL-MAEEGVPAPLPPEDAPNAASLAPTPVSPVLEPFNLTSEPSDYA 142
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                                                                                                                                                                                                                                                                                                                                                                               18;
                                                                                                                                                                                                                                                                                                                                                                                                     9.2%;
Similarity 39.1%;
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1206
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larity 39.1%;
Conservative
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29, LAST SEQUENCE UI
35, LAST ANNOTATION
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864
970
981
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133464 MW;
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163809 MW; 42CA4104 CRC32;
                         PROTEIN DELTA (C/EBP
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Pred. No. 1.44e-01;
15; Mismatches 9
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Pred. No. 1.44e-01;
15; Mismatches 9
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POLY-SER.
PRO-RICH.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ALTERNATIVE SPECING
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Best Local S
Matches 10
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p46694;
01-NOV-1995 (REL. 32, CREATED)
01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)
01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
RADIATION-INDUCIBLE IMMEDIATE-EARLY GENE IEX-1 (IMMEDI
PROTEIN GLY96) (IMMEDIATE EARLY RESPONSE 3 PROTEIN).
PROTEIN GLY96) (IMMEDIATE EARLY RESPONSE 3 PROTEIN).
IEX1 OR GLY96 OR IER3.
MUS MUSCULUS (MOUSE).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; M
                                                                01-NOV-1990 (REL 16, CREAT

01-NOV-1990 (REL 16, LAST;

01-FEB-1991 (REL 17, LAST;

VIRAL PROTEIN TPX.

THERMOPROTEUS TENAX VIRUS 1

VIRIDAE; DS-DNA ENVELOPED V
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TRANSMEM
DOMAIN
CARBOHYD
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CHARLES C.H., YOON J.K., SIMSKE J.S., LAU L.F.;
ONCOGENE 8:797-801(1993).
-!- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN (POTENTIAL)
-!- TISSUE SPECIFICITY: EXPRESSED PREDOMINANTLY IN THE LUNG, T
SEQUENCE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PIR;
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P19275;
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STRAIN-BALB/C;
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INDUCTION: BY SERUM GROWTH FACTORS
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MGI:104814; IER3
                                                                                                                                                                                                                                                                                                                                 EPISAPITAPPVLEPLNLTSESSDYALDLKAFI 153
| :|: |-||||:||||:||| :||
AP--TPVS--PVLEPFNLTSEPSDYALDLSTFL 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APTPVSPVLEPFNLTSEPSDYALDLSTFLQQHPAAF 156
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90245666.
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86
103
137
153 AA;
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1 85

86 102

103 153

103 153
                                                                                                                                                                                                                                       STANDARD;
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LAST SEQUENCE UF
LAST ANNOTATION
                                                                   1 (STRAIN VT3) (TTV1) VIRUSES; LIPOTHRIXVIR:
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Pred. No. 1.15e-120;
22; Mismatches 19:
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POTENTIAL.
EXTRACELLULAR (POTENTIAL).
POTENTIAL.
7A284EC2 CRC32;
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                                                                     LIPOTHRIXVIRIDAE
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Matches 2
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Best Local S
Matches 2
                                                                                       YO25_CAEEL
P34675;
O1-FEB-1994
O1-FEB-1994
O1-JUN-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                             010442;
01-NOV-1997
01-NOV-1997
01-NOV-1997
                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
MEISSNER J.D., HIRSCH G.N., LARUE E.A., FULCHER R.A.,
SUBMITTED (MAY-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
EMBL; U95843; G2072333; -
CORE PROTEIN; LATE PROTEIN.
SEQUENCE 228 AA; 25571 MW; DE97BB3A CRC32;
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SEQUENCE
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NUCLEIC ACIDS RES. 18:2171-2171(1990).
EMBL; X14717; E20711; -.
PIR; S06686; S06686.
PIR; S15921; S15921.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REPEAT
REPEAT
REPEAT
SEQUENCE FROM N.A. STRAIN-BRISTOL N2; MEDLINE; 94150718.
                                            CAENORHABDITIS ELEGANS EUKARYOTA; METAZOA; ACC
                                                                              HYPOTHETICAL
                                                                                                                                                                                                                                                                                                                                                                                                                                   MINOR CORE PROTEIN (PROTEIN V).
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                                                                                                                                                                                                                                                                                                                                                                                                 MOUSE ADENOVIRUS TYPE 1 (MAV-1).
VIRIDAE; DS-DNA NONENVELOPED VIRUSES; ADENOVIRIDAE;
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                                                                                                                                                                                                      VERRRRVAQTVPVVRYHPSIQVEPAVHPPLAP 212
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                                                                                                                                                                                                                             PSTIPGPRRGSGPEIFTFDPLPEPAAAPAGRPSASRGHRKRSRRVLYPRVVRRQLPVEEP
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474 AA;
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(REL.
                                                                           (REL. 28, CREATED)
(REL. 28, LAST SEQUENCE UPDATE)
(REL. 29, LAST ANNOTATION UPDAT
L 202.6 KD PROTEIN ZK688.5 IN CH
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llarity 29.3%;
Conservative
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                                                                                                                                    STANDARD;
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35, LAST SEQUENCE UPDATE)
35, LAST ANNOTATION UPDATE)
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377
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                                            ACOELOMATES;
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Pred. No. 9.76e-03;
21; Mismatches 41
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BAC5D831 CRC32;
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                                            NEMATODA; SECERNENTEA; RHABDITIDA
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IN CHROMOSOME
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Release 3.0.4A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1997 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd.

rch_pp protein - protein database search, using Smith-Waterman algorithm

Tabular output not generated. Fri Apr 17 13:38:32 1998; MasPar time 6.24 Seconds 626.917 Million cell updates/sec

Description: Perfect Score: Title:

Sequence: >US-08-799-910-10 (1-156) from US08799910.pep 11114 1 MCHSRSCHPTMTILQAPTPA......EPSDYALDLSTFLQQHPAAF 156

Scoring table: PAM 150 Gap 11

Searched: 69112 seqs, 25083644 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database: swiss-prot35 1:swiss1

Statistics: Mean 44.412; Variance 91.621; scale 0.485

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

No.	Score	Query Match	Length	DB B	ID	Description	Pred. No
ببر	1102	98.9	156	_ ;	IEX1_HUMAN	RADIATION-INDUCIBLE IM	5.97e-
2	752		153	ب	<u>, </u>	IBLE	
ω	117	\circ	7	Ь	VTP3_TTV1V		
4	112	10.1	228	ப	VCOM_ADEM1		9.76e-0
5	. 109	9.8	1799	<u>_</u>	YO25_CAEEL		
6	103	9.2	1206	,_	FOR4 MOUSE	\circ	
7	103	9.2	1468	ب	FORM_MOUSE	FORMIN (LIMB DEFORMITY	1.44e-01
œ	101	9	268	-	CEBD_RAT	CCAAT/ENHANCER BINDING	
9	101	9	417	L	Alab_Canfa	ALPHA-1B ADRENERGIC RE	
10	101		816		QA1F_NEUCR	QUINIC ACID UTILIZATIO	2.57e-01
11	99	8	272	H	GSPC_ERWCH	SEC	
12	98	80	272	۳	GSQC_ERWCH	GENERAL SECRETION PATH	6.05e-01
13	98	8	390	L	VGLI_HSV11	GLYCOPROTEIN I.	6.05e-01
14	98	8	475	۳	GAPN_STRMU	NADP-DEPENDENT GLYCERA	6.05e
15	98	œ	519	ப	A1AB_HUMAN	ALPHA-1B ADRENERGIC RE	6.05e-01
16	98	8	975	<u>-</u> -	CDP_CANEA	CCAAT DISPLACEMENT PRO	6.05e-01
17	97	ထ	1043	ب	CHS2_PARBR	CHITIN SYNTHASE 2 (EC	
18	97	89	1239	-ب	V120_EBV	PR	
19	97	89	1337	_	PTPJ_HUMAN	PROTEIN-TYROSINE PHOSP	8.02e-01
20	96	80	245	ب	VE4_HPV5B	PROBABLE E4 PROTEIN.	1.06e+00
21	96	80	245	ا	VE4_HPV05	PROBABLE E4 PROTEIN.	1.06e+00
22	96	8.6	1233	_	NAMES CLWD	CAMPA DECE	1.06e+00
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45	44	43	42	41	40	39	38	37	36	35	34	ω ω	32	31	30	29	28	27	26	25	24
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440	1692	926	820	631	620	517	464	350	276	268	232	1742	389	279	217	3866	643	534	493	449	316
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YW19_MYCTU	POLN_HEVPA	YIK9_YEAST	FIBL_HUMAN	DMK_MOUSE	EXTN_TOBAC	MBEA_ECOLI	SP62_HUMAN	Y08N_MYCTU	YIT4_YEAST	CEBD_MOUSE	SAX1_CHICK	GUNA_CALSA	NDPP_MOUSE	AOAANT160A	YKR4_EBV	HRX_MOUSE	VP40_HSVE2	APG_ARATH	GUNA_XANCP	APG_BRANA	CDNC_HUMAN
HYPOTHETICAL 45.3 KD T	NON-STRUCTURAL POLYPRO	HYPOTHETICAL 103.6 KD	FIBRINOGEN-LIKE PROTEI	MYOTONIN-PROTEIN KINAS	EXTENSIN PRECURSOR (CE	MOBILIZATION PROTEIN M	SPLICEOSOME ASSOCIATED	HYPOTHETICAL 37.0 KD P	HYPOTHETICAL 31.3 KD P	CCAAT/ENHANCER BINDING	HOMEOBOX PROTEIN SAX-1	ENDOGLUCANASE A PRECUR	NPC DERIVED PROLINE RI	HYPOTHETICAL 29.3 KD P	HYPOTHETICAL BKRF4 PRO	ZINC FINGER PROTEIN HR	CAPSID PROTEIN P40 (CO	ANTER-SPECIFIC PROLINE	MAJOR EXTRACELLULAR EN	ANTER-SPECIFIC PROLINE	CYCLIN-DEPENDENT KINAS
4.15e+00	3.17e+00	3.17e+00	3.17e+00	3.17e+00	3.17e+00	2.42e+00	2.42e+00		2.42e+00	2.42e+00	2.42e+00		1.84e+00	1.84e+00		1.40e+00	1.40e+00	1.40e+00	1.40e+00	NE 1.40e+00	1.40e+00

ALIGNMENTS

AF012089 Drosophila melanogaste 3.32e-03 T18278 Sequence 5 from patent 2.61e-02 GGU41467 Gallus gallus fibrobla 1.36e+00 SSL36LBP S.crofa mRNA for L-36 1.36e+00 BOVIOPP Bovine inorganic pyrop 1.36e+00 DIRHSP70 Dirofilaria immitis 70 1.36e+00 MM26SPROT Mus musculus mRNA for 1.36e+00 XLU69669 Xenopus laevis nuclear 1.36e+00		C 7 8 9 10 11 11 11 11 11 11 11 11 11 11 11 11
M.musculus gly96 mRNA. 1 R.norvegicus PRG1 gene 3 Sequence 14 from paten 1 Sequence 15 from patent 5 Sequence 5 from patent 5		00 - 4480
ID Description Pred. No.	Query Query Core Match Length DB	Result No. Sc
f results predicted by chance to have a all to the score of the result being printed, s of the total score distribution.	. No. is the number of r greater than or equal is derived by analysis o	Pred. score and is
Variance 7.667; scale 1.489	: Mean 11.417;	Statistics
om 16:gb_ov 17:gb_in 18:gb_pl 19 vi 22:gb_ph 23:gb_sy 24:gb_un 29	15:	Database:
lor 3:em_om 4:em_ov 5:em_pl 6:em_htg em_hum2 9:em_ba 10:em_ro 11:em_un 12:em_vi	8 : eg	Database:
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91221332 bases x 2	354530 seqs, 5	Searched:
y 0	TD': Dbase 0; Query	Nmatch S
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799-910-9) from USO8799910.seq ATGTGTCACTCTCGCAGCTGAAAAAAAAAAAAAA	>US-08- (1-1228 : 1228 : 1	Title: Description: Perfect Score N.A. Sequence Comp:
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1444 2240 2498 2842 3016 6258 8595 27471	714 714 861 979	1435 1908 2031 2179 2179 2301 2624 2628 5061 38890 38890 38890	3042 3042 3217 3737 3789 571 1404	1840
17 17 17 17 17	16	125 125 125 125 125 125 125 125 125	15 18 14 16 16	17
LCU56636 MAU43333 A26375 DDU31631 PFSC03080 DDU14576 CELC44C3	MMKOKCS BVBETV1B AF025506 S78789S4	DMU75652 MMRNASEB4 MMFPHROM E08204 RNU75903 AF020409 I66342 DDU75144 CELC15144 CELC15144	SC11545 SX11545 ZMU85494 S78355 XELMYBRP1 SCU41441 S76875	DDU73686
Lucilia cuprina alpha Lucilia cuprina alpha Mesocricetus auratus 5 RING4 coding sequence. Dictyostelium discoide Plasmodium falciparum Dictyostelium discoide Caenorhabditis elegans	B.verrucosa Bet v 1b m Rattus norvegicus pren CGATA-3 [chickens, liv	ebanogastebla mana or prothror prothror galpha 2gicus UDp m discoid rom paten discoid is elegan thaliana is elegan	RNA for in ON1 protea in D1 (mic evis myb-r melanogas	ostelium dis
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ALIGNMENTS

Db 712 A	Query Match Best Local Matches 1	BASE COUNT ORIGIN	FEATURES	JOURNAL MEDLINE	AUTHORS	TITLE JOURNAL	REFERENCE	NID KEYWORDS SOURCE ORGANISM	RESULT 1 LOCUS DEFINITION ACCESSION
712 ATGTGCCACTCGCGCAACCATCTCCACACACATGACTGGCCTGAGGGCCCCTTCTCCAGCT 771	y Match 9.6%; Score 118; DB 14; Length 1938; Local Similarity 77.8%; Pred. No. 1.49e-48; nes 165; Conservative 0; Mismatches 47; Indels 0; Gaps 0;	390 a	-	glycosylated protein Oncogene 8 (3), 797-801 (1993) 93173526	Charles, C.H., Yoon, J.K., Simske, J.S. and Lau, L.F. Charles, C.H., Yoon, J.K., Simske, J.S. and Lau, L.F. Genomic structure, cDNA sequence, and expression of gly96, a growth factor-inducible immediate-early gene encoding a short-lived	Direct Submission Submitted (29-JUL-1992) L. Lau, University of Indinois College of Med., Dept. of Genetics, M/C 669, 808 South Wood Street, Chicago, IL 60612, USA 2 (bases 1 to 1938)	Eukaryotae; mitochondriai eukaryotes; metazoa; chordata; Vertebrata; Eutheria; Rodentia; Sciurognathi; Myomorpha; Muridae; Murinae; Mus. 1 (bases 1 to 1938) Lau.L.	9287803 gly96 gene; glycosylated protein. house mouse. Mus musculus	MMGLY96 1938 bp RNA ROD 11-MAR-1993 M.musculus gly96 mRNA. x67644

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JOURNAL
MEDLINE
REFERENCE
AUTHORS
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JOURNAL
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TITLE
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Best Local Similarity 76.9%;
Matches 163; Conservative
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               CGCAGCCGACGGGTGCTCTACCCTCGAGTGGT 801
                                                      CTCCCGGACCCCCAGCGGCCCCTGCCGGGCGCCCCAGCGCCTCTCGCGGGCACCGAAAG
                                                                                                              CCCTCCACCGGCCCGGAACTCCGGCGGGGGCTCCGGGTCCCGGAATTTTCACCTTCGACCCC 709
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                                                                                   CTCCCGGAGCGGGCGGTAGCGTCCGCCGTGCGTCCGAACACTTCTCGCGGGCACGGAAAA 769
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 CGCAGCCGCAGGGTTCTCTACCCTCGAGTGGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (05-MAR-1996) A. Trauzold, Laboratory of Gastroenterology, 1st Dept.of Medicine, University Schittenhelmstrasse 12, Kiel, D-24105, FRG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Schafer, H., Trauzold, A., Siegel, E.G., Folsch, U.R. and Schmidt, W.E. PRG1: a novel early-response gene transcriptionally induced by pituitary adenylate cyclase activating polypeptide in a pancreatic carcinoma cell line
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Norway rat.
Rattus norvegicus
Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Rodentia; Sciurognathi; Muridae; M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Direct Submission
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590. 1279
/gene="PRG1"
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/db_xxef="taxon:10116"
/cell_line="AR4-2J"
590. .1279
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gene.
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Pred. No. 3.33e-46;
0; Mismatches 49;
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                                                                                                                                                                                                                                                                                                                                                     CCAGCTGCCAGTCGAGGAACCGAACCCAGCCAAAAGGCTTCTCTTCTGCTGCTCACCAT 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GCCCCCTTCT
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                                                                                                                                                                                                                                                                                                                                                                                                                        CGTCTTCTGCCAGATCCTGATGGCTGAAGAGGGTGTGCCCGGCGCCCCTGCCTCCAGAGGA 338
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Unknown.
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Dorner, F., Scheiflinger, F. and Falkner, F. Gunter.
Recombinant fowlpox virus
Patent: US '5670367-A 14 23-SEP-1997;
                                                                                                                                                                Unknown
                                                                                                                                                                           Unknown
                                                                                                                                                                                                Sequence 14 from I66494 g2724471
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Dorner, F., Scheiflinger, F. and Falkner, F. Gunter.
Recombinant fowlpox virus
Patent: US 5670367-A 14 23-SEP-1997;
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Sequence 14 from patent US 5670367.
I66494
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h 5.5%;
Similarity 2.4%;
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Score 67; DB 25; L
Pred. No. 1.82e-19;
214; Mismatches 156;
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Pred. No. 4.27e-26;
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                                                                                                                 196 GNKRDVSSYANNKCCGSSC 214
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                                                                                                                                                                                                                                   TCACAGTTAG-AAGGCGGCCGGGTGTTGCTGGAGGAAAGTGCTGAGGTCCAGAGCGTAGT 419
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128278
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Bennett,A., Labavich,J.M., Powell,A. and Stotz,H.
Plant inhibitors of fungal polygalacturonases and their use
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  control fungal disease Patent: US 5569830-A 5 29-OCT-1996;
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ilarity 18.1%;
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8 c 25 g
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Pred. No. 5.19e-06;
79; Mismatches 80;
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Eukaryotae; mitochondrial eukaryotes; Metazoa; Arthropoda;
Tracheata, Hexapoda; Insecta; Pterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
1 (bases 4546 to 4553)
Gray, Y. H., Tanaka, M.M. and Sved, J.A.
P-element-induced recombination in Drosophila melanogaster: h;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (30-JUN-1997) School of Biological Sciences, University of Sydney, Biology Al2, Sydney University, NSW 2006, Australia Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3 (bases 1 to 10772)
Gray, Y.H.M., Sved, J.A.,
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gray,Y.H.M., Sved,J.A., Preston,C.R. and Engels,W.R. Structure of the cysteine proteinase (CP1) gene of Drosophila melanogaster and associated mutational effects
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unpublished
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/gene="CP1"
4546. .4553
/gene="CP1"
                                                                                                                                                                                                                                                                                                                                                                                          /db.xref="pid:q2305221"
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/translation="MRTAVLLPLALLAVAQAVSFADVVMEEWHTFKLEHRKNYQDET
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QLRAADESFKGVTFISPAHVTLPKSVDWRTKGAVTAVKDQGHCGSCWAFSSTGALEGO
QHFRKSGVLVSLSEQNIVDCSTKYGNNGCNGGLMDNAFRYIKDNGGIDTEKSYPTEAID
DSCHFNKGTVGATDRGFTDIPQGDEKKMAEAVATVGPVSVAIDASHESFQFYSEGVYN
                                                                                                                 /gene-"CP1"
6751. .7707
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/db_xref="taxon:7227"
join(872. 1000,2310. .2426,6476. .
/product="phenylalanyl tRNA synthetase"
join(8110. .9300,9370. .>9532)
/note="potential orf"
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/gene="CP1"
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                                                                                               'gene="CP1
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'gene="CP1"
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Local Similarity 18.1%;
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Gray, Y.H.M., Sved, J.A., Preston, C.R. and Engels, W.R.
Structure of the cysteine proteinase (CP1) gene of Drosophila
melanogaster and associated mutational effects
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                                                                                                                                                                                                                                                                                     of Sydney, Biology Al2, Sydn
Location/Qualifiers
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P-element-induced recombination in Drosophila melanogaster: hybrid
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Tracheata; Hexapoda; Insecta; Prerygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila
1 (bases 4546 to 4553)
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YFKDNWLEVLGCGIMRHEILQRSGVHQSIGYAFGVGLERLAMVLFDIPDIRLFWSNDS
GFLSQFSEKDLHNLPKYKPISHYPQCTNDLSFWLPQDIEVDAGFSPNDFYDLVRSVAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /translation="MLLTLRVQGARHWIKSTRCLASSAAPAKSPSSPPQLEVSGSTYA
TDGWTRVTPKILSYVGANKHLQTDHPLSIIRQRIVNZYGAGYRYQRGNPLFSVYDQMN
PVVTVQQNEDHLLIRADHVSROKSDCYYINQOHLLRAHTTAHQVELISGELDNELVVE
EVYRRDEIDSTHYPVFHQADAVRLVTKDKLFERNPGLELFEETWSGTLADPKLILPHP
2310. .2426
/gene="CP1"
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/gene="CP1"
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                                                                                             'gene="CP1"
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/product="phen
                                                                                                                                                                     product="cysteine protease"
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|PID:q2305222"
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Pred. No. 4.03e-04;
57; Mismatches 27; Indels
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                                                                                                                                                                                                                                                                                                                                                                               TIGCATAAGTTAAAATAATTACGTACA-CATCTCCATCACCTAGGAGGACGTACATA 751
                                                                                                                                                                                                                                         Sequence 5 from patent US 5569830.
                Bennett, A., Labavitch, J.M., Powell, A. and Stot Plant inhibitors of fungal polygalacturonases control fungal disease Patent: US 5569830-A 5 29-OCT-1996;
                                                                                                                                                                                                                      g1819054
                                                                                                                               Unclassified
                                                                                                                                                         Unknown
                                                                                                                                                                              Unknown
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Similarity 19.0%;
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/gene="CP1"

4546. 4553

/gene="CP1"

/note="insertion site of P{CaSpeR}(50C)"
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PVVTVQQNFDNLLIPADHYSROKSDCYYINQQHLLRAHTAHQVELISGGLDNFLVVG
EVYRRDEIDSTHYPVFHQADAVRLVTKDKLFERNPGLELFTAHGYETLADPKLILPHP
SSWYKRNSPATRRAVKLMEHEMKHVLVGLTKDLFGPRIKYRWVDTYFPFTQPSWELEI
YFKDNWLEVLGCGIMRHEILQRSGVHQSIGYAFGVGLERLAMVLFDIPDIRLFWSNDS
GFLSQFSEKDLHNLPKYKPISHYPQCTNDLSFWLPQDIEVDAGFSPNDFYDLVRSVAG
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eerfrlkifnenkklakhnorfaegkvsfklavnkyadlihestockhofstytihk
olraadesfkovtfispahvtlpksvumktkoavtavkogchoeschafsstgalego
hfrksgvlyslseonlydcstkygnngcngglmdnafryikdnggidteksyfyeaid
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/gene="CP1"
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join(8110. .9300,9370. .>9532)
/note="potential orf"
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EPQCDAQNLDHGVLVVGFGTDESGEDYWLVKNSWGTTWGDKGFIKMLRNKENQCGIAS
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/db_xref="PID:g2305221"
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/gene="CP1"
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Pred. No. 3.32e-03;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          859 TGAGCTTTGTGGGACTGGTGGAAGCAGGACACCTGGAACTGCGGCAAAGTAGGAGAAGAA
                                979 TAAGTTTAGGAGGTGACTGCATCCT 1003
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                                                                                    Local
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 GGU41467
Gallus gallus
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Similarity 12.2%;
25; Conservation
                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (27-NOV-1995) Philip H. Cross:
Parnassus, San Francisco, CA 94143-045,
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Archosauria; Aves; Neognathae; Galliformes;
Phasianidae; Phasianinae; Gallus.
1 (bases 1 to 800)
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                                                                                    Similarity
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                                                                                                                                             /product="fibroblast growth factor 8 FGF8"
/db_xref="PID:g1134970"
/translation="VFWHLFVLCLQAQVTVQSPPNFTQHVREQSLVTDQLSRRLVRTY
CLYSRTSGKHVQILDNKKINAMAEDGDVHAKLIVETDTFGSRVRIKGAATGFYICMNK
KGKLIGKSNGKGKDCVFTEIVLENNYTALQNAKYEGWYMAFTRKGRPRKGSKTRQHQR
EVHFMKRLPKGHQTTEPHRRFEFLNYPFNRRSKRTRNSSARVRP"
a 219 c 226 g 130 t
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                                                                                                                                                                                                                                                                                                              /tissue_type="brain"
                                                                                                                                                                                                                                                                                                                                   /dev_stage="embryo"
                                                                                                                                                                                                                                                                                                                                                   /organism="Gallus gallus"
/db_xref="taxon:9031"
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fibroblast
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                                                                 Score 29;
Pred. No.
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Pred. No. 2.61e-02;
79; Mismatches 101
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1.36e+00;
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l (bases 1 to 1266)
Yang, Z. and Wensel, T.G.
Molecular cloning and functional expression mammalian inorganic pyrophosphatase
J. Biol. Chem. 267, 24641-24647 (1992)
93077559
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S.scrofa mRNA
X79303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (18-MAY-1994) E.J. O'Keefe, University of 137 NCMH, Dept of Dermatology, CB7600, Chapel Hill, Location/Qualifiers
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                                                                                                                                                                        Bos taurus
                                                                                                                                                                                      inorganic pyrophosphatase.
Bos taurus retina cDNA to mRNA.
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Bovine inorganic pyrophosphatase
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Vertebrata; Eutheria; Artiodactyla; Suiformes; Suina; Suidae;
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                                                                                                                                Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Artiodactyla; Ruminantia; Pecora;
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lu,M.L., Parry,D.A.,
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/product="1-36 lactose binding protein"
/product="1-36 lactose binding protein"
/db_xref="prD:g623346"
/translation="MAFVPAPGYQPTYNPTLPYYKPIPGGLRVGMSVYIQGVANEHMK
/franslation="MAFVPAPGYQPTYNPTLPYYKPIPGGLRVGMSVYIQGVANEHMK
RFTVNIFVVGQCPGADVAFHFNPRFDGMVKVYNSQQDGXMGNEEKKRSWPFRKAPAFE
LVIMVLPEHYKVVVNGDPFYEFGHRIPVQLVTHLQVGGDLTAQSINFIGGQPAPSPGP
MPNGYPGGFGKHNQQPCNLPCMEGAPTFNPPVPYKTRLQGGLVARRTIYIKGYVPPSG
KSLYINFKVGSSGDVALHINPRLTEGIVVRNSYLNGKWGAEEKKSSFNPFAPGQYFDL
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347 c 303 g 220 t
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49. .1020
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Sus scrofa"
/db_xref="taxon:9823"
/dev_stage="adult"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /gene-"1361bp"
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/cell_type="keratinocyte"
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of L-36 lactose binding
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Pred. No. 1.36e+00;
0; Mismatches 4
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                                                                                                                                                                                                                                                                  mRNA sequence
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NC 27514, USA
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26S proteasome;
complex.
                                                                     Mus musculus
Y13071
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Culpepper, J.A., Friedman, L. and Dale, B.
Molecular cloning and characterization of a Dirofilaria immitis
cDNA encoding an Hsp 70 homologue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               heat shock protein 70; heat shock protein homologue Dirofilaria immitis adult cDNA to mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DIRHSP70 1294 bp mRNA INV 25-AUG-1992 Dirofilaria immitis 70 kDa heat shock protein homologue (hsp 70)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryotae; mitochondrial eukaryotes; Metazoa; Nematoda; Secernentea; Spiruria; Spirurida; Spirurina; Filarioidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Dirofilaria immitis
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                                                                                                 MM26SPROT
             house mouse
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musculus
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llarity 87.2%;
Conservative
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                                                                                                                                                                                                                                                                                                                          /codon_start=1
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/product="heat shock protein 70"
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LSGIPPAPRGVPQIEVTFDIDANGILNVSAQDKSTGKQNLTITINDKGRLSKDEIERM
LSGIPPAPRGVPQIEVTFDIDANGILNVSAQDKTGTFNFKTNKTGFDNKKKTOFKCDE
                                                                                                                                                                                                                                                                                                         TVRWLDGNQTAEKDEFEHRQKELESVCNPIITKLYQSAGGMPGGMPGGMPGGAPGGGS
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/db_xref="taxon:9913"
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239 c 300 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Dirofilaria immitis"
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                                                                                                                                                                                                                                                                                                                                                                                                                                      'note="homologue"
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                                      non-ATPase subunit;
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Pred. No. 1.36e+00;
0; Mismatches 5
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Pred. No. 1.36e+00;
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                                    proteolysis; regulatory
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Gordon,C.

Direct Submission
Submitted (08-MAY-1997) C. Gordon,
Developmental Genetics, Western Gr
Edinburgh EH4 2XU, UK
Location/Qualifiers
1479
                                                                  Cordes, V.C., Hunzicker, A. and Landson Direct Submission
Submitted (06-SEP-1996) Cell Biology/0110, Center, INF 280, Heidelberg 69120, Germany
                                                                                                                                                                                                                             Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea Pipidae; Xenopodinae; Xenopous.

1 (bases 1 to 1811)
1 (cordes, V.C., Reidenbach, S., Rackwitz, H.R. and Franke, W.W. Cordes, V.C., Reidenbach, S., Rackwitz, H.R. and Franke, W.W. Identification of protein p270/Tpr as a constitutive component the nuclear pore complex attached intranuclear filaments J. Cell Biol. 136 (3), 515-529 (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                African clawed frog 
Xenopus laevis
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Similarity 87.2%;
34; Conservation
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                                             1. .1811
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translation="MDRLLRLGGGMPGLARPPTDAPAVDTAPOVYISSLALLKMLKHG/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QDPKRHLEEHVDVLMTSNIVQCLAAMLDTVVFK"
270 c 349 g 407 t
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/db_xref="PID:e352083"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /db_xref="taxon:10090"
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Pred. No. 1.36e+00;
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protein TPR (tpr)
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U73686
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                                                                                                                                                                                                                                                                                                                                      Submitted (08-OCT-1996) Anatomy & Cell Biology, University of Florida, 1600 SW Archer Rd., Gainesville, FL 32610-0235, USA Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                  West,M.C., Kozarov,E. and Teng-umnuay,P. Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                            98038971
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          acid position
Gene 200 (1-2), 1-10 (1997)
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The cytosolic glycoprotein FP21 of Dictyostelium discoideum is encoded by two genes resulting in a polymorphism at a single amino
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryotae; Dictyosteliida; Dictyostelium 1 (bases 1 to 1840)
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Dictyostelium discoideum
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llarity 78.4%;
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STGNVPTSVDSGAADEGDEVFVEAESEGIGAESTLEMDTQQEEPVQPSEADLPSTSQD
PPSSSIADTSSSKPKPRRVMLQPQPGGRPFKRSRGGSDFRGRGGINRSNI"
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<1. .1678
                                                                                                                                                                                                               1061. .1703
/gene="fpa2"
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NVTSTILEKVLDYCRHHHQHPSPQGDDKKDEKRLDDIPPYDRDFCKVDQPTLFELILA
ANYLDIKPLLDVTCKTVANMIRGKTPEEIRKIFNIKNDFTPEEEEQIRKENEWCEDKG
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GTDPDTETEDSMTAGEGNQRAADSQNIGDSGVVTAESTFSQETREQPSSASDRQGPRP
PQSPRRQAHPPRLTILAPPQELGPPPAQRIPVARRQSVGRGLQLTPGVGGMQHFFDEE
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/note="nuclear pore complex-associated protein;
translocated promotor region"
                                                                                                                                                                      /organism-"Dictyostelium discoideum"
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/clone_lib="Uni-ZAPTMXR library, Stratagene"
                                                                                                  /product="cytosolic glycoprotein FP21"
/db_xref="PID:g1658024"
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  1158. .1311
                                                                                                                                       /codon_start=1
                                                                                                                                                          note="SKP1-like; similar to the product of the fpal gene"
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'translation="vQPTQQSHATIESPTQETPVEIVQSSPVERPTTSSTFGTYSATP
'SSIPKRPREEEEDSTIETPEQIADDTDQQRTKKEKEEDIEEKTEBAUHI
'ROCSNMEFPLEEEIVESPIQTSQVIESQAPEQLANGSTQDSLQDTPPKKTHNLVV
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Pred. No. 1.36e+00;
0; Mismatches 11
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                                          2.4%;
Similarity 87.2%;
34; Conservation
                                                                                                         /gene="fpa2"
742 a 166 c
                                             Score 29; DB 17; L
Pred. No. 1.36e+00;
0; Mismatches 5;
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rights by rights by 139:41 199 0-9 050879991 050879991 050879991 050879991 050879991 050879991 050879991 050879991 050879991 0708799962 b 08 08 09 08 09 08 09 09 09 0708799962 b 0708799962 b 08 08 08 08 08 08 08 08 08 08 08 08 08	. Collins
aspar time 157.52 Se MasPar time 157.52 Se Million cell part1 5:part5 6:part 11:part11 12:part12 12:part2 7:part12 11:part11 12:part12 11:part11 12:part12 11:part11 12:part12 11:part11 12:part12 11:part11 13:part12 12:part2 23:par 13:part2 23:par 12:part2 23:par 13:part2 23:par 12:part2 23:par 13:part2 23:par 12:part2 23:par 13:part2 23:par 13:part2 23:par 13:part2 23:par 12:part2 23:par 13:part2 23:par 12:part2 23:par 12:par 12:part2 23:par 12:par 12:p	h, u. K.
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.57e-	.57e-0	.57e-0	.57e-0	.92e-0	.20e-0	.08e-0	1.05e-03 1.05e-03 2.93e-03 2.93e-03 2.93e-03	.74e-0 .74e-0 .74e-0 .74e-0	.74e-

ALIGNMENTS

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RESULT 1

ID 7534; standard; DNA; 297 BP.

AC 077534;

AC 077535;

AC 077534;

AC 077535;

AC 077535;

AC 077535;

AC 077535;

AC 077536;

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 /label= N-glycos_site
Modified -site 244..246
/label= N-glycos_site
Modified -site 277.279
/label= N-glycos_site
Modified -site 349.351
 Natriuretic protein receptor B - for diagnosis and treatment of kidney failure, heart failure, hyperaldosteronism, glaucoma etc. Claim 3; Fig 1; 49pp; English.

The sequence was derived from the DNA encoding natriuretic peptide receptor B, NPRB, having guanyl cyclase (GC) activity and protein kinase activity. The DNA can be inserted into expression vectors for the prodn. of the protein, opt. after being mutated to produce NPRB analogues. The protein has a mol wt. of 115 kD (calculated Mr. 114,952). The protein has a mol wt. of solate peptides using affinity chromatography. Antibodies with affinity for NPRB can also be prepd.
 (GETH) GENENTECH INC.
Chang M, Goeddel D, Lowe
WPI; 91-036711/05.
N-PSDB; Q10324.
 /note= "GC and protien kinase
Modified -site 24.26
/label= N-glycos_site
Modified -site 35.37
 09-APR-1991 (first entry)
Human Natriuretic Peptide Receptor B.
NPRB; ANP; BNP; CNP; kidney failure;
hyperaldosteronism; glaucoma; guanyl
 IT 2
Q10572 standard;
Q10572;
 /label= n-gl:
wo9100292-A.
 /label= n-glycos_site
Modified -site 600..602
 /label= N-glycos_site
Modified -site 195..197
 /label= N-glycos_site
Modified -site 161..163
 22-JUN-1990; U03586.
23-JUN-1989; US-370673.
 /note= "binds natriuretic peptides
Domain 456..456
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 /label=
 Homo sapiens.
 'label≖ extracellular domain
 'label- mature
 187
 127
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 GCCAAAAGGCTTCTCTTTCTGCTGCTCACCATC
 tccaggaatctctaccctagagtgatccggcgccagttgccagttaagggaccaaacctc
 GAGCCCGCAGCGGCCCCTGCCGGGCGCCCCAGCCCCTCTCGCGGGCACCGAAAGCGCAGC
 N-glycos_site
 479..1047 cytoplasmic domain
 signal
 1047 BP;
 sequence
 Location/Qualifiers
 DNA;
 87
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Α.,
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 activity"
15
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 A, B
 cyclase
 heart failure;
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 Query Match
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Matches
 1197
 1017
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 959
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 841
 662
 543
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 900
 553
 782
 494
 722
 435
 376
 602
 316
 256
 483
 196
 423
 136
 364 CCCACCCCTGTGTCCCCCGTCCTCGAGCCCTTTAATCTGACTTCGGAGCCCTCGGA-CTA
 304 GAAGAGGGTGTGCCGGCGCCCCTGCCTCCAGAGGACGCCCCTAACGCCGCATCCCTGGCG
 76
 16
 Local Similarity 9.0%;
nes 83; Conservative
 TTACTGTCAAAAAAAAAAAAAAAA
 mvvsgnngrngnrhannnarmana
 TCCGTCTGTCTACTGTGTGAGACTTCGGCGGACCATTAGGAATGAGATCCGTGAGATCCT
 nnddnnanyakknntannnnsgnnnnttgmnaadvysngnnnnnnanrsgppynngndns
 CGGCAAAGTAGGAGAAATG-GGGAGGACTCGGGTGGGGAGGACGTCCCGGCTGGGA
 CTGTCACGGAGCGACTGTCGAGATCGCCTAGTATGTTCTGTGAACACAAATAAAATTGAT
 nanandsvtnynsdnvgntansanstnmnvvtnnndnytcndanndnndvykvntngday
 ggtsnndnnnnrmnnyannnnknvnnrtnaynnnkrkanannynnnnhsvannnkrgntv
 nknnvnkvrngnrnynrnsndrtnnnnnnvnnmnrcwandnanrndngnnkgnnrrnnkn
 TGAAGT-CTGGTGGT-GGGTCGTAAGTTTAGGAGGTGACTGCATCCTCCAGCATCTCAAC
 nnndwmnrysnnndnvkgmannhnsnnsshgsnkssncvvdsrnvnkntdygnasnrsta
 AGGTCTCTTGGTATTTATTGAGCTTTGTGG-GACTGGTGGAAGCAGGACACCTGGAACTG
 vnkkrnnntrnvnnnnkhmrdvnnnhntrnngacndnnnncnvtnycnrgsnndnnnnds
 TACGTAATATTTATTTAACTTATGCAAGGGTGTGAGATGTTCCCTCTGC-TGTAAATGC
 nrwnnnngnsnryhkgagsrn-tnsnrgssygsnmtahgkynnnantghnkgnvvankh
 dnnncandnddnscdktnnstnanvangtgntnnmngvssnnnnrknmnnknnasmn-wr
 vtgnvvmdknndrntdnvnwamgdndsgdnnnaahysganknnww-tgrnnnwvkganns
 rarndngvnngnsnmnnnagcnydgnnnyanvnnntnnnggtrndgnrnvnkmngrryhg
 AGAGCGTATCCCCAACTGGGACTTCCGAGGCA-ACTTGAACTCAGAACACTACAGCGGAG
 dvngnsnragntratgrnwndnrtrnnananrnanntvnvntyrnnnnnnynnnnnrnnn
 CGCACTCCCCAAAAAGAATCCGAAAAACCACAAAGAAACACCAGGCGTACCTGGTGCGCG
 CGCTCTGGACCTCAGCACTTTCCTCCAGCAACACCCGGCCGCCTTCTAACTGTGACTCCC
 gvrnngarnntnavvnnnhnnsyawawnrvgnavanavnangrannvdnrnvssnnngac 75
 TCCATCTTCTTGAAGTCGCCTTTAGGGTGGCTGCGAGGTAGAGGGTTGGGGGGTTGGTGGG
 ATTGCTCCTAATTAATATTTATATGTATTTATGTACGTCCTCCTAGGTGATGGAGATGTG
 ACGCCACCCGGTGCTTGAGGCCGGACCGAGGCGCACAGAGACCGAGGCGCATAGAGACCG
 snynannsavdnknyhdndnnngngcvynaasvarnashwrnnnntagavasgnsakndh
 7.7%;
 ; Score 94; Di
; Pred. No. 5.!
263; Mismatcl
 936
 ne 94; DB 2; L
1. No. 5.93e-35;
Mismatches 568
 Length 1047;
 Indels
 10;
 Gaps
 1076
 1136
 1016
 434
 422
 135
 363
 912
 958
 672
 899
 612
 840
 552
 781
 493
 601
 542
 482
 792
 721
 661
 375
 315
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RESULT ID Q AC Q DT 09

Q10572 standard; Q10572; 09-APR-1991 (fi

DNA;

1047

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 Query Match
Best Local Similarity
Matches 75; Conser
 (GETH) GENENTECH INC. Chang M, Goeddel D, Lov WPI; 91-036711/05. N-PSDB; Q10324
 /label cytoplasmic domain 's
/note- "GC and protien kinase activity"
Modified site 24..26
 Natriuretic protein receptor B - for diagnosis and treatment of kidney failure, heart failure, hyperaldosteronism, glaucoma etc. Claim 3; Fig 1: 49pp; English.
The sequence was derived from the DNA encoding natriuretic peptide receptor B, NPRB, having guanyl cyclase (GC) activity and protein kinase activity. The DNA can be inserted into expression vectors for the prodn. of the protein, opt. after being mutated to produce MPRB analogues. The protein has a mol wt. of 115 kD (calculated Mr=114,952). The protein (or variants) can be used in treatment of natriuretic peptide disorders, and also to isolate peptides using affinity chromatography. Antibodies with affinity for NPRB can
 Modified
 /label= n-glycos_site
Modified -site 349..351
 /label= N-glycos_site
Modified -site 277..279
 /label= N-glycos_site
Modified -site 244..246
 /label= N-glycos_site
Modified -site 195..197
 Modified
 /label= N-glycos_site
Modified -site 35..3
 Doma i n
 Domain
 Human Natriuretic Peptide Receptor B. NPRB; ANP; BNP; CNP; kidney failure;
 also be
 22-JUN-1990;
23-JUN-1989;
 /label- N-glycos_site
Modified -site 161..163
 10-JAN-1
 /label= transmembrane domain
 /label= extracellular domain
 /label=
 lomo sapiens
 hyperaldosteronism; glaucoma; guanyl
 878
 208
 148
 89
 29
 CTCACACCCTTGCATAAGTTAAAATAATATTACGTACACATCTCCATCACCTAGGAGGA
 vvnnnhnnsyawawnrvgnavanavnangrannvdnrnvssnnngacsnynannsavdnk
CACCAGTCCCACAAAGCTCAATAAATACCAAGAGACCTGCATTTACAGCAGAGGGAACAT
 kngnnvvtnhghnnwtaraannyndartddrnhyntnngvnnanngsnnsvnhnvyarnn
 "binds natriuretic peptides 456..456
 prepd.
 N-glycos_site
d -site 600..6
 mature
 signal
 N-glycos_site
 U03586.
US-370673.
 Conservative
 NPBR
 sequence
 B₽;
 479..1047
 Location/Qualifiers
 D, Lowe
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 8.5%;
 87
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 Score 80; DB 2; Lei
Pred. No. 2.20e-27;
248; Mismatches 546;
 15 C;
 A
B
 cyclase.
 heart failure; protein kinase;
 83
 C,
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 Length 1047;
 Indels
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 Gaps
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 88
 207
 10;
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 Q77554 s
 New nucleic acid fragment encoding gene products - can he for genetic analysis and mapping Claim 1; Page 586; 616pp; English.

Human nucleic acid fragments, isolated from brain, adren the placenta or bone marrow comprise any of: (A) a seque selected from (Q76401-Q77613), (B) an allelic variation sequence as described in (A), or (C) a sequence complements.
 20-JAN-1994.
13-JUL-1993; G01467.
13-JUL-1992; GB-014857.
(MEDI-) MEDICAL RES COUNCIL.
Gross J. Hadfield KM, Howells
 Human genome fragment. (Prereizeu,
Brain; placenta; bone marrow; genetic analysis;
Brain; placenta; homology; human; adrenal tissue; ds.
 Sibson DR, Starkey M; WPI; 94-035056/04.
 WO9401548-A.
 Homo sapiens.
 sequence known
 Preferred sequences exhibit
 23-SEP-1994
 400
 506
 460
 446
 520
 386
 580
 327
 640
 268
 700
 864
 624
 340
 564
 103
 804
 163
 222
 684
 280
 43
 (A) or
 CTCCTTCCCACCGGGCCTAGCCCCAGCTGGGCTGTGCCTCGGTCTCTATGCGCCTCGGTC
 nndnvkgmannhnsnnsshgsnkssncvvdsrnvnkntdygnasnrstannddnnanyak
 ryhkga-gsrntnsnrg-ssygsnmtahgkynnnantghnkgnvvankhvnkkrnnntrn
 nscdktnnstnanvangtgntnnmngvssnnnnrknmnnknnasmnwrnrwnnnnngnsn
 ratg-rnwndnrtrnnananrnanntvnvntyrnnnnnnynnnnnrnnnrarndngvnng
 CGTCCTCTGGAGGCAGGGGGGCACACCCTCTTCAGCCATCAGGATCTGGCAGAAGA
 vnnnnkhmrdvnnnhntrnngacndnnnncnvtnycnrgsnndnnnndsnnndwmnrysn
 GATTAAAGGGCTCGAGGACGGGGGACACAGGGGTGGGGCGCCAGGGATGCGGCGTTAGGGG
 CCGGGTGTTGCTGGAGGAAAGTGCTGAGGTCCAGAGCGTAGTCCGAGGGCTCCGAAGTCA
 TTTCTTTGTGGTTTTTCGGATTCTTTTGGGGAGTGCGGGGAGTCACAGTTAGAAGGCGG
 ndrntdnvnwamgdndsgdnnnaahysganknnwwtgrnnnwvkgannsdnnncandndd
 TCAAGTTGCCTCGGAAGTCCCAGTTGGGGATACGCTCTCGCGCACCAGGTACGCCTGGTG
 nsnmnnnagcnydgnnnyanvnnntnnnggtrndgnrnvn-kmngrryhgvtgnvvmdkn
 TCTGTGCGCCTCGGTCCCGCCTCAAGCACCGGGTGGCGTCTCCGCTGTAGTGTTCTGAGT
 GCAGGATGGTCATGGTCGGGTGGCAGCTGCGAGAGTGAC
 nsdnvgntansanstnmnvvtnnndnytcndanndnndv
 rmnnyannnnknvnnrtnaynnnkrkanannynnnnhsvannnkrgntvnanandsvtny
 AGGCGCTGGGGCCCCGGCAGGGGCCGCTGCGGGCTCCGGGAGAGGGTCGAAGGTGAAGA
 nrnynrnsndrtnnnnnnvnnmnrcwandnanrndngnnkgnnrrnnknggtsnndnnnn
 CTGGCGCCGGACCACTCGAGGGTA-GAGAACCCTGCGGCTGCGCTTTCGGTGCCCGCGAG
 TCTCAGGACCGGAGCCCCGCCGGGGTCCCGGGATGGTGGAGGGGGCCCGGGGTCGGGGCCT
 knntannnnsgnnnnttgmnaadvysngnnnnnanrsgnnynngndnsnknnvnkvrng
 standard; DNA;
 (B)
 (first entry)
fragment. (Preferred)
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 (C) a sequence complementary
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 902
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 gene mapping;
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 623
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 401
 505
 461
 521
 385
 581
 863
 683
 281
 341
 104
 803
 164
 223
 743
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RESULT
ID QI
AC QI
DT 3:
DE 0
KW 0
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 A single-stranded DNA (or its complementary strand or the corresp. C double-stranded DNA) which comprises one of the 7837 "GS" sequences given in T19001-T26837 and which is able to hybridise to part of thuman genomic DNA, cDNA or mRNA is claimed. The GS (Gene Signature) sequences were obtained from 3'-directed cDNA libraries prepared from various human tissues; synthesis of cDNA was initiated from the GS 'end of mRNA by using poly(T) as the sole primer. Since the 3'-cuntranslated sequence is unique to a particular mRNA species, almost all the 3'-oriented cDNAs hybridise with specific mRNAs. Each library is constructed so as to reflect accurately the relative abundance of different mRNAs in the particular tissue from which it was derived. The appearance frequency of a given GS in a cDNA library can be gequences) as a means of diagnosing abnormal cell function or for recognising different cell types.

Sequence 53 BP; 18 A; 9 C; 9 G; 17 T;
 Query Match
Best Local S
Matches 4
 Query Match
OLT 6
Q51746 standard; cDNA; 91 BP.
Q51746;
31-MAY-1994 (first entry)
Oligonucleotide probe MK14-A
Oligonucleotide; DNA probe; my
 Matsubara K, Okubo K;
WPI; 95-206931/27
Identifying gene signatures in for diagnosis of abnormal cell
 1158
 Human gene signature HUMGS02013.
Gene signature; messenger RNA; mRNA; relative abundance; human; cloning; mapping; non-biased library; diagnosis; ccell typing; abnormal cell function; ss.
 01-JUN-1995.
11-NOV-1994; J01916.
12-NOV-1993; JP-355504.
 Claim 1; Page 723; 224
A single-stranded DNA
 Sequence
 (MATS/) MATSUBARA K. (OKUB/) OKUBO K.
 09-JUL-1996 (first entry)
 T20789
 tissues
 233
 217
 Local
 ccctagctgctagtcgagaatcegaactccgc
 aactcgt-tcacacgcgccgaaagcctattcccaggactctctgcccctacgtga-ccgn
 CGCCAGCTGCCAGTCGAGGAACCGAACCCAGC
 AGCGCCTCTCGCGGGCACCGAAAGCCGCAGCCGCAGGGTTCTCTACCCTCGAGTGGTCCGG
 standard;
 l Similarity
114; Conser
 h 3.8%;
Similarity 100.0%;
47; Conservative
 267
 5.0%;
llarity 75.0%;
Conservative
 BP;
 CDNA
 2245pp;
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 58
 mRNA;
 Score 47;
Pred. No.
0; Misma
mycobacteria;
 Score
Pred.
0; M
 3'-directed human cDNA library -
function, by preparing cDNA that
corresp. mRNA in specific human
 53
 117
 Mismatches
 Mismatches
 No.;
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 DB 18;
2.61e-10;
 DB lu,
6.80e-18;
 248
 264
 49
 disease
 0
 Length 53;
 Length
 Indels
 Indels
 42
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 frequency;
 0
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 Gaps
 Gaps
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 232
 156
 174
 0
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RESULT RESULT PROSESSION OF STANDARD PROSESSI
 RESULT
ID NO
AC NO
AC NO
DT OS
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KW E
OS ES
FH K6
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 Query Match
Best Local S
Matches
 Query Match
Best Local
 Matches
 Q51746 standa
Q51746;
31-MAY-1994
 ss.
Synthetic.
Synthetic.
 1153
 WPI; 93-3788447...
New oligo:nucleotide probes
Astection and amplification
 N81164; standard; DNA; 204 BP.
N81164;
N8-NOV-1990 (first entry)
Base substituted E.coli beta-galactosidase alpha-fragment.
E.coli beta galactosidase alpha-fragment; base substitutio
Escherichia coli
 Claim 3; Page 14; 23pp; English.

Oligonucleotide probe MK14-A consists of nucleotides 5-95 of (Q51735). It hybridized to all spp. of mycobacteria tested, cross reacted to a few non-mycobacterial spp. The probe may be useful as an initial screen for mycobacterial infection. See also Q51735-45 and Q51747-59.

Sequence 91 BP; 5 A; 17 C; 15 G; 4 T;
 Claim 3; Page 14; 23pp; English.
Claim 3; Page 14; 23pp; English.
Oligonucleotide probe MK14-A consists of nucleotides 5-95 of (051735). It hybridized to all spp. of mycobacteria tested, cross reacted to a few non-mycobacterial spp. The probe may be useful as an initial screen for mycobacterial infection. See also Q51735-45 and Q51747-59.
Sequence 91 BP; 5 A; 17 C; 15 G; 4 T;
 (BECT) BECTON DICKINSON Shank DD, Spears PA; WPI; 93-378844/48.
 (BECT) BECTON DICKINSON Shank DD, Spears PA; WPI; 93-378844/48.
 Key
 EP-571911-A.
01-DEC-1993.
24-MAY-1993; 108325.
26-MAY-1992; US-889651
 Oligonucleotide probe MK14-A Oligonucleotide; DNA probe; r
 New oligo:nucleotide probes detection and amplification
 EP-571911-A.
01-DEC-1993.
24-MAY-1993; 108325.
26-MAY-1992; US-889651
 samples
 Synthetic
 samples
 isc_feature
 13
 88
 CAGTCGCTCCGTGACAGCCCACCAACCCCAACCCTCTACCTCGCAGCC
 vhsyyvvhvvshhhsvhhvvhhvhvsvvvvhhvvhhvhhvhyhvyvsvc
 ggctccggcgssvhsyyvvhvvshhhsvhhvvhvvsvvvvhhvvhvvhhvhyhvyvsv
 GGCTCCGGTCCTGAGATCTTCACCTTCGACCCTCTCCCGGAGCCCGCAGCGGCCCCTGCC
 standard;
 Similarity
 Similarity
 8
 3.5%;
larity 2.0%;
Conservative
 3.7%;
larity 13.3%;
Conservative
 (first
Location/Qualifiers
 entry)
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 ВP
 specific for Mycobacteria of Mycobacteria
 Score
Pred.
45; M
 specific for Mycobacteria of Mycobacteria nucleic ac
 mycobacteria;
 Score 46; DB 9; I
Pred: No. 8.07e-10;
45; Mismatches
 Mismatches
 43; DB 9; I
No. 2.31e-08;
 disease
 Length
 Length
 substitutions;
 diagnosis;
 Indels
 acid
 acid
 91;
 91;
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 Gaps
 Gaps
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 Matches
 Query Match
 EP-265123-A.
05-MAY 1988, 105163.
30-MAR 1988; 105163.
03-APR-1987; US-034819.
(SUSO) SUOMEN KOKERI OY.
LEHTOVGATE P, KNOWES J,
WPI; 88-279927/40
 Random point mutations were introduced into the alpha fragment of E.coli beta-galactosidase. The wild type sequence was obtained as a single stranded template and an ollgonucleotide was hybridised to it to generate a popn of DNA molecules which terminate at all possible nucleotide positions within a specified region. The variable 3' ends generated in this way are used as primers for reverse transcriptase. Nucleotides are misincorporated by the transcriptase and the molecules are completed to forms that can be amplified and then expressed in a suitable host-vector system. The sequence covers all 176 difft base substitutions, most of which
 Introducing random point mutations into nuby prepn of single stranded template, annomisincorporation, completion of molecules
Disclosure; p; English.

Disclosure; p; English.

Random point mutations were introduced into the alpha fragment Random point mutations were introduced into the alpha fragment Random point mutations were introduced into the alpha fragment Random point mutations were introduced into the alpha fragment Random point was hybridised template and an oligonucleotide was hybridised
 EP-285123-A.

05-MAY-1988.
00-MAY-1988: 105163.
03-ARR-1987; US-034819.
(SUSO) SUOMEN SOKERI OY.
Lehtovaara P. Knowles J. Koivula A. Bamford J. Reinikainen WPI; 88-279927/40.
 Introducing random point mutations into nucleic by prepn of single stranded template, annealing misincorporation, completion of molecules and so
 Escherichia
 08-NOV-1990 (first entry)
Base substituted E.coli beta-galactosidase alpha-fragment.
E.coli beta galactosidase alpha-fragment; base substitution
 1075
 1134 CACCAACCCCAACCCTCTACCTCGCAGCCACCCTAAAGGCGACTTCAAGAAGA-TGGAA 1076
 occurred singularly in any given mutant.
See also P80575.
Sequence 204 BP; 21 A; 47 C; 17
 Disclosure; p; English.
 primer_bind
 misc_feature
 N81164 standard;
N81164;
 primer_bind
 /function=multiple cloning site
primer_bind 187..204
 1015 TTGA 1012
 /function=multiple cloning
 /*tag=
 /*tag=
 182
 62
 Local
 kydccynachhddhyvybbbvynvhnhnncncccbnnhvchnvhbnnhrnwayvrhdarr 181
 ddvh
 ywccgagcycgaayycdchvgccgymrttthhyrrmrbnvyrdynrsdaaawyccyrrsv
 Similarity
 18;
 185
 galactosidase alpha-fragment;
coli.
 Conservative
 Location/Qualifiers 19..69
 DNA;
 187..204
 3.5%;
 204
 J, Koivula
 ВР
 site
 Score
Pred.
61; M
 Þ,
 Mismatches
 No 43
 Bamford
 to nucleic acods -
annealing a primer,
ules and screening.
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annealing a primer,
ules and screening.
 B
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 base substitutions;
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 44;
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 Length
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PT Identifying proteins or peptide(s) which bind a ligand - by proteins or peptide(s) which bind a ligand - by screening a recombinant vector library expressing fusion proteins procedure of comprising a binding domain and an effector domain proteins procedure; page 35; 255pp; English.

PS Disclosure; page 35; 255pp; 25; 25pp; Query Match
Best Local
 Matches
 it to generate a popn of DNA molecules which terminate at all possible nucleotide positions within a specified region. The variable 3 'ends generated in this way are used as primers for reverse transcriptase. Nucleotides are misincorporated by the transcriptase and the molecules are completed to forms that can be amplified and then expressed in a suitable host-vector system. The sequence covers all 176 difft base substitutions, most of which
 (UYNC-) UNIV NORTH C. Fowlkes DM, Kay BK; WPI; 94-279739/34.
 Generic DNA sequence to generate a random TSAR peptide library TSAR; totally synthetic affinity reagent; synthetic; binding defector domain; concateneated heterofunctional protein; linker direct; rapid; detection; screening; treatment; generic; ss.
 occurred singularly in any given mutant. See also P80575.
 01-FEB-1993; US-013416.
30-DEC-1993; US-176500.
31-JAN-1994; US-189331.
 Q70469 standard;
 Sequence
 WO9418318-A.
 sequence
 /note- "this
 Synthetic.
 07-APR-1995
 070469
 144 nvhnhnncncccbnnhvchnvhbnnhrnwayvrhd
 66
 84
 24
 9
 Match
 cyyrcayrccbgcaggycgacbcyrraggnyccccgggywccgagcycgaayycdchvgc
 _feature
 GGAGCCCGCAGCGGCCCCTGCCGGGCGCCCCCAGCG
 CACCATCCCGGGACCCCGGGGGGGCTCCGGTCCTGAGATCTTCACCTTCGACCCTCTCCC
 cgymrttthhyrrmrbnvyrdynrsdaaawyccyrrsvkydccynachhddhyvybbbvy
 CTCTCGCAGCTGCCACCCGACCATGACCATCCTGCAGGCCCCGACCCCGGCCCC-CTC--
 rapid; detection;
 Similarity
29; Conser
 O.F
 204 BP;
 σ
 sequence represents '2'; .
 (first entry)
 Conservative
 Location/Qualifiers 55..60
 DNA;
 CAROLINA
 3.3%;
 21 A;
 Score 41; DB 1;
Pred. No. 2.10e-07
69; Mismatches 5
 47 C;
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 178
 160
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 54;
 11
 Length
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 Indels
 108
 3
 Others;
 linker;
 domain;
 Gaps
 65
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Query Match
Best Local Similarity
"---hes 11; Conserv
 ç
 PT Identifying process or peptide(s) which bind a ligand - by
PT screening a recombinant vector library expressing fusion proteins
PT comprising a binding domain and an effector domain
PS Disclosure; Page 36; 255pp; English.
CC (700,72 is a generic DNA sequence used to generate random TSAR (Totally
CC Synthetic Affinity Reagents) peptides.This generic formula can also be
CC (CAC)(NNB)5(CAC)2(NNB)4. X and Y are flanking restriction sites
CC (X is not the same as Y) that are not specified further. The peptides
CC (X is not the same as Y) that are not specified further. The peptides
CC (X is not the same as Y) that are not specified further. The peptides
CC concatenated by this and other generic sequences (70,040,73) have invariant
CC concatenated heterofunctional proteins or peptides, comprising at least
CC uncutonal regions - a binding domain with affinity for a ligand and
CC active. They may further comprise a linker peptide between the 2 domains
CC vivo to deliver a chemically or biologically active moiety, eg. metal
CC vivo to deliver a chemically or biologically active moiety, eg. metal
CC ion, radioisotope, peptide, toxin or enzyme, to the specific target or
CC monoclonal or polyclonal antibodies and therefore circumvent the need
CC monoclonal or polyclonal antibodies and therefore circumvent the need
CC complex methods of hybridoma formation or in vivo antibody
CC activity allowing direct and rapid detection in a screening process.
SO Sequence 114 BP; 6 A; 12 C; 0 G; 0 T;
 င္မ
 g
 В
 8888888
 Query Match
 01-FEB-1994; U00977.
01-FEB-1993; US-013416.
30-DEC-1993; US-176500.
31-JAN-1994; US-189331.
 Generic DNA sequence to generate a random TSAR peptide library. TSAR; totally synthetic affinity reagent; synthetic; binding domain; effector domain; concatenated heterofunctional protein; linker;
 or enzyme, to the specific target or on the cell. They can also replace the function of macromolecules, eg. monoclonal or polyclonal antibodies and therefore circumvent the need for complex methods of hybridoma formation or in vivo antibody production. The TSARs are easily characterised and have designed activity allowing direct and rapid
 (UYNC-) UNIV NORTH Fowlkes DM, Kay BF WPI; 94-279739/34.
 .T 11
Q70472 standard; DNA; 114
 direct; rapid;
 detection in a screening
 P-PSDB; R58383
 18-AUG-1994.
 WO9418318-A
 misc_feature
 Synthetic.
 /note= "encoded
 10-APR-1995
 643 GTCTCTGTGCGCCTCGGTCCCGCCTCAAGCACCGGGTGGCGTCTCCGCTGT
 703 GCTCTCCTTCCCACCGGGCCTAGCCCAGCTGGGCTGTGCCTCGGTCTCTATGCGCCTCG
 Local Similarity
 2 gcnnbnnbnnbnnbnnbnnbnnbnnbnnbnnbtgcnnbnnbnnbnnbnnbnnbnnnnnn
 114 BP;
 2.9%;
llarity 10.1%;
Conservative
 Kay BK;
 3.0%;
ilarity 6.3%;
Conservative
 (first entry)
 detection; screening;
 γģ
 Location/Qualifiers 55..60
 0
 process.
 ВP
 Score 37;
Pred. No.
32; Misma
 Score 35; DB 12;
Pred. No. 1.32e-04;
29; Mismatches 69
 4 C;
 Mismatches
 DB 12; Len
. 1.59e-05;
. hes 72;
 4
റ;
 4 T;
 Length 114;
 Length 114;
 Indels
 112
 0
 0;
 Gaps
 61
 0
 0
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g,
 Сþ
 PT Identifying proteins or peptide(s) which bind a ligand - by screening a recombinant vector library expressing fusion proteins pT comprising a binding domain and an effector domain Disclosure; Page 35; 255pp; English.

CC O70468 is a generic DNA sequence used to generate random TSAR (Totally O70468 is a generic DNA sequence used to generate formula can also be represented as follows: X(NNB)11(TGC)(NNB)62(NNB)107 X X CC and Y are flanking restriction sites (X is not the same as Y) that are cont specified further. Other generic sequences are shown in Q70466-68.

CC Other specific peptides generated by these generic sequences are shown in CC comprising at least two functional regions - a binding domain with CC chemically or biologically active. They may further comprise a linker peptide between the 2 domains. The oligonucleotides are also designed so that the expressed peptide contains 2 or 4 cysteine residues. These residues confer some degree of conformational rigidity to the peptides. The TSARs or dealing domain can be used in vivo to deliver a chemically or biologically active moiety, eg. metal ion, cradicisotope, peptide, toxin or enzyme, to the specific target or on the cell. They can also replace the function of macromoleules, eg. monoclonal or polyclonal antibodies and therefore circumvent the need for complex methods of hybridoma formation or in vivo antibody sequence 114 BP; 0 A; 2 C; 2 G; 2 T;
 В
 Вb
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 Qγ
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 Query Match
Best Local
 Matches
 01-FEB-1993; US-013416.
30-DEC-1993; US-176500.
31-JAN-1994; US-189331.
(UYNC-) UNIV NORTH CAROLIFOWIKES DM, KAY BK;
WPI; 94-279739/34.
 Q70468
 effector domain;
direct; rapid; d
 Generic DNA sequence to generate a random TSAR petide library. TSAR; totally synthetic affinity reagent; synthetic; binding ceffector domain; concateneated heterofunctional protein; linke
 P-PSDB; R65154
 comments) "
 sequence of
 Synthetic.
 05-APR-1995
 Q70468
 WO9418318-A.
 misc_feature
 18-AUG-1994
 /note- "this
 642
 702
 141
 63
 Local Similarity
 66
 81
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 bnnbnnbnnbnnbnnbnnbnnbnnbtgcnnbnnbnnbnnbnnbnnnnnnnn
 CCCTGCCGGGCGCCCAGCGCCTCTCGCGGGCACCGAAAGCGCAGCCGC 189
 bnnbnnbnnbnnbnnbtgcnnbnnbnnbnnbnnbnnbnnbnnbnnbnnbnnb
 bnnbnnbnnbcacnnbnnbnnbnnbcaccacnnbnnbnnbnnb
 CCGGCGGGGCTCCGGAGATCTTCACCTTCGACCCTCTCCCGGAGCCCGCAGCGGC
TCTCTGTGCGCCTCGGTCCCGCCTCAAGCACCGGGTGGCGTCTCCGCTGTAG
 standard;
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 sequence represents 'Z';
5, 9 or 12 nucleotides (so
 Conservative
 (first entry)
 detection;
 Location/Qualifiers 55..60
 DNA;
 CAROLINA
 2.9%;
3.6%;
 screening;
 Score 36; DB 12;
Pred. No. 4.59e-05;
34; Mismatches 7:
 (see
 treatment;
 2
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 74;
 Length 114;
 | protein;
| generic;
 Indels
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 0;
 Gaps
 62
 δ5
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RESULT PROCESS OF THE SULT AC OF DE GE
 Identifying proteins or peptide(s) which bind a ligand - by screening a recombinant vector library expressing fusion proteins proteins proceeding a pinding domain and an effector domain proteins proceeding a binding domain and an effector domain proteins processing a binding domain and an effector domain proteins processing a pinding domain and an effector domain proteins proteins or particles. Page 35; 255pp; English.

CC 070467 is a generic DNA sequence used to generate random TSAR (Totally CC graph of the peptides of the peptides formula can also be represented as follows: x(NNB)16(TGC)(NNB)12(NNB)16(TGC)(NNB)12 (NNB)16 (TGC)(NNB)12 (NNB)16 (TGC)(NNB)12 (NNB)16 (TGC)(NNB)12 (NNB)16 (TGC)(NNB)12 (NNB)16 (TGC)(NNB)16 (TGC)
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Best Local Similarity
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 18-AUG-1994.

01-FEB-1994; U00977.

01-FEB-1993; US-013416.

30-DEC-1993; US-176500.

31-JAN-1994; US-189331.
 LT 13
Q70467 standard; DNA; 114 BP.
Q70467;
 Generic DAN sequence to generate a random TSAR petide library.
TSAR; totally synthetic affinity reagent; synthetic; binding dom:
effector domain; concateneated heterofunctional protein; linker;
direct; rapid; detection; screening; treatment; generic; ss.
 comments
 7 14
070466 standard; DNA; 114 BP.
070466;
05-APR-1995 (first entry)
 (UYNC-) UNIV NORTH
Fowlkes DM, Kay BI
WPI; 94-279739/34.
 WO9418318-A.
 sequence
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 Synthetic.
 05-APR-1995
 P-PSDB; R65153
 Generic DNA sequence
 636
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 TGCGCCTCGGTCCCGCCTCAAGCACCGGGTGGCGTCTCCGCTGTAGTG
 TTCCCACCGGGCCTAGCCCCAGCTGGGCTGTGCCTCGGTCTCTATGCGCCTCGGTCTCTG 637
 114 BP;
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 Kay BK;
 sequence represents 'Z'; Z
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 Conservative
 Location/Qualifiers 55..60
 CAROLINA.
 2.98;
to generate
 0 A;
 Score 36; DB 12;
Pred. No. 4.59e-05;
33; Mismatches 71
 a screening 2 C; 2 G;
 a random TSAR-9 petide library
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 71; Indels
 Length 114;
 0
 domain;
 Gaps
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B
 PT Identifying proteins or peptide(s) which bind a ligand - by screening a recombinant vector library expressing fusion proteins proceeding a binding domain and an effector domain proteins procedure; Page 35; 255pp; English.

CC Synthetic Affility Reagents) peptides. This generic formula can also be comprising a fility Reagents) peptides. This generic formula can also be compresented as follows:XNNBJ1(TGC)(NNBJ10(TGC)2(NNB)4Z
 Matches
 Query Match
Best Local
 18-AUG-1994.
01-FEB-1994; U00977.
01-FEB-1993; US-013416.
30-DEC-1993; US-175500.
31-JAN-1994; US-189331.
(UYNC-) UNIV NORTH CAROLJ
FOWLKES DM, KAY BK;
WPI; 94-279739/34.
p-PSDB; R65152.
 TSAR; totally synthetic affinity reagent; synthetic; binding domain; effector domain; concateneated heterofunctional protein; linker; direct; rapid; detection; screening; treatment; generic; ss.
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 misc_feature
 W09418318-A.
 Synthetic.
 /note= "this
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Similarity
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 sequence represents '2';
6, 9 or 12 nucleotides (se
 Conservative
 Location/Qualifiers 55..60
 or 12 nucleotides (see
 2.9%;
 Score 36; DB 12; Length 114.
Pred. No. 4.59e-05; Pr.
31; Mismatches 71; Indels
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 Length 114;
 0;
 Gaps
 64
 for
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H K D D Z Z O D P B C D D
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19-DEC-1996.
06-JUN-1996;
07-JUN-1995;
 T76405;
 chronic obstructive synthetic.
 Asthma;
 WO9640162-A1.
 Human endothelin-1
 15-SEP-1997
 643
 703
 65 nbnnbnnbnnbnnbnnbtgcnnbnnbnnbnnbnnbnnbnnbnnbnnb
 GTCTCTGTGCGCCTCGGTCCCGCCTCAAGCACCGGGTGGCGTCTCCGCTG
 GCTCTCCTTCCCACCGGGCCTAGCCCCAGCTGGGCTGTGCCTCGGTCTCTATGCGCCTCG
 standard;
 ndothelin-1 antisense oligonucleotide.
airway epithelium; adenosine free; cystic fibrosis;
 (first entry)
U09306.
US-474497
 DNA;
 pulmonary
 disease; bronchitis;
```

```
pr Mettger WJ, Nyce JW;

DR MPI; 97-051817/05.

PT Treatment of airway diseases such as asthma - by topically applying adenosine-free antisense oligo:nucleotide to airway epithelium of pr subject subject produced. CC which involves the topical administration of an essentially adenosine free antisense oligonucleotide (ON) to the airway epithelium of the cC which involves the topical administration of an essentially adenosine free antisense oligonucleotide (ON) to the airway epithelium of the cC subject. The present sequence is an antisense oligonucleotide for the human endothelin-1, targeted at the initiation codon. The cC asthma, chronic obstructive pulmonary disease such as cystic fibrosis, CC airway diseases characterised by an inflammatory response. By clinicating adenosine from the antisense ON, its liberation upon called bronchocomstriction in patients with hyper-reactive airways. So sequence 178 Bp; OA; Score 35; DB 31; Length 178; Best Local Similarity 28.2%; Pred. No. 1.32-04; Matches 20; Conservative 33; Mismatches 18; Indels 0; Gaps 0; Matches 20; Conservative 33; Mismatches 18; Indels 0; Gaps 0; 500 CCGGGCCTAGCCCCAGCTGGGCTGTGCCCTCGGTCTCTATGCCCCTCGGTCTCTGTGCGCC 631

Db 105 cbbgccbcbcbcbgcbgbbbbbcbcbgcbgbbbbcbctcbgcbbbbbbbccccc 175

Cp 630 TCGGTCCCGCC 620

Search completed: Thu Apr 23 05:42:23 1998
```

(MT)

Release 3.0.4A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1997 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

MPsrch\_pp protein - protein database search, using Smith-Waterman algorithm

Tabular output not generated. Fri Apr 17 13:41:02 1998; MasPar time 6.99 Seconds 310.069 Million cell updates/sec

Title:

Description: Perfect Score: >US-08-799-910-10
(1-156) from US08799910.pep
1114

1 MCHSRSCHPTMTILQAPTPA.....EPSDYALDLSTFLQQHPAAF 156

Scoring table:

Searched: PAM 150 Gap 11 111726 seqs, 13889129 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

a-geneseq30
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18
19:part19 20:part20 21:part21 22:part22 23:part23

Statistics: Mean 31.062; Variance 153.160; scale 0.203

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

| 6 8.6 1239 12 R66064<br>8.6 1244 12 R66061<br>5 8.5 198 10 R59841<br>5 8.5 198 15 R92113<br>5 8.5 311 10 R59843<br>8 8.5 311 15 R92115<br>8 8.4 167 23 W14574<br>8 8.4 206 23 W14574                                                                                                    | ;        | Score<br>1001<br>1001<br>98<br>98<br>98<br>98<br>99<br>97<br>97<br>96 | <br>1 | DB 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 | W14570<br>R528150<br>R528150<br>R52831<br>R52831<br>R52831<br>R65943<br>R65943<br>R65057<br>R65057<br>R65065<br>R65065<br>R65063<br>R65063 | Streptococcus pneumon Sygar beet chitinase Alpha 1b adrenergic r Sequence of human alp Alpha-1B adrenergic r Sequencecus pneumon hubep-1. Human NMDAR2 receptor |
|-----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|----------|-----------------------------------------------------------------------|-------|------------------------------------------|--------------------------------------------------------------------------------------------------------------------------------------------|-----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 6 8.6 1219 12 R66063<br>6 8.6 1219 12 R66063<br>6 8.6 1231 12 R66062<br>6 8.6 1236 12 R66037<br>6 8.6 1239 12 R66064<br>6 8.6 1244 12 R66061<br>8 8.5 1244 12 R66061<br>1 8.5 198 10 R59841<br>5 8.5 198 15 R92113<br>5 8.5 311 10 R59843<br>5 8.5 311 10 R59843<br>6 8.4 167 23 W14575 |          | 600000                                                                |       | 21499                                    | R53072<br>R52831<br>R85943<br>W14569<br>R85203<br>R85203                                                                                   | Alpha<br>Sequen<br>Alpha-<br>Strepto<br>huDEP-<br>Human                                                                                                                                                                                                                                             |
| 8.6 1236 12 R66064<br>8.6 1239 12 R66064<br>8.6 1244 12 R66061<br>8.5 198 10 R59841<br>8.5 198 15 R92113<br>8.5 311 10 R59843<br>8.5 311 15 R92115<br>8.4 167 23 W14574<br>8.4 206 23 W14574                                                                                            |          | 96                                                                    |       | 222                                      | R66065                                                                                                                                     |                                                                                                                                                                                                                                                                                                     |
| 6 8.6 1244 12 R66001<br>8.6 124 12 R66001<br>5 8.5 198 10 R59841<br>5 8.5 198 15 R92113<br>5 8.5 311 10 R59843<br>5 8.5 311 10 R59843<br>6 8.4 167 23 W14575<br>8 8.4 206 23 W14575                                                                                                     |          | 9 6                                                                   |       | 25                                       | R66037                                                                                                                                     | Human                                                                                                                                                                                                                                                                                               |
| 95 8.5 198 10 R59841<br>95 8.5 198 15 R02113<br>95 8.5 311 10 R59843<br>95 8.5 311 15 R02115<br>94 8.4 167 23 W14574<br>94 8.4 206 23 W14574                                                                                                                                            |          | 96                                                                    |       | 12                                       | R66061                                                                                                                                     | Human NMDAR2                                                                                                                                                                                                                                                                                        |
| 95 8.5 311 10 R59843<br>95 8.5 311 15 R92115<br>94 8.4 167 23 W14575<br>94 8.4 206 23 W14574                                                                                                                                                                                            | 16       | 95<br>50<br>50                                                        |       | 15                                       | R59841<br>R92113                                                                                                                           | ApoE4L protease Human ApoE4L.                                                                                                                                                                                                                                                                       |
| 94 8.4 167 23 W14575<br>94 8.4 206 23 W14574                                                                                                                                                                                                                                            | 17<br>18 | 95<br>95                                                              | 11    | 10                                       | R59843<br>R92115                                                                                                                           | ApoE4Lx2 prote<br>Human ApoE4Lx2                                                                                                                                                                                                                                                                    |
|                                                                                                                                                                                                                                                                                         | 20       | 9.4<br>4.4                                                            |       | 233                                      | W14575                                                                                                                                     | Streptococcus                                                                                                                                                                                                                                                                                       |

| 4.4<br>5.4                                     | 43                    | 42     | 41                    | 40                    | 39     | 38<br>8 | 37                    | 36       | ω<br>G | 34       | ω<br>ω                | 32     | 31                    | 30     | 29                   | 28                    | 27                    | 26                    | 25                    | 24             | 23                    | 22       | 21                    |
|------------------------------------------------|-----------------------|--------|-----------------------|-----------------------|--------|---------|-----------------------|----------|--------|----------|-----------------------|--------|-----------------------|--------|----------------------|-----------------------|-----------------------|-----------------------|-----------------------|----------------|-----------------------|----------|-----------------------|
| 87<br>87                                       | 87                    | 87     | 87                    | 87                    | 89     | 89      | 89                    | 89       | 90     | 90       | 90                    | 90     | 90                    | 90     | 91                   | 9                     | 91                    | 92                    | 92                    | 92             | 92                    | 93       | 92                    |
| 7.8<br>7.8                                     |                       |        |                       |                       |        |         |                       |          |        |          |                       |        |                       |        |                      |                       |                       |                       |                       | ٠              | •                     | •        |                       |
| 1784<br>1784                                   | 1442                  | 294    | 278                   | 170                   | 915    | 858     | 609                   | 269      | 610    | 610      | 610                   | 610    | 388                   | 294    | 289                  | 147                   | 129                   | 1693                  | 1693                  | 1247           | 254                   | 183      | 166:                  |
| 16                                             | 13                    | 17     | 17                    | 17                    | 21     | Ö       | σ                     | 7        | 16     | φ        | 9                     | 22     | ü                     | u      | æ                    | 1                     | 23                    | 18                    | 9                     | 14             | N                     | ω        | 23                    |
| tn 🕰                                           | R79480                | R96991 | R94965                | W00498                | W14013 | R30477  | R32131                | R40801   | R89436 | R56664   | R51116                | W18201 | R78734                | R78729 | R52633               | R60799                | W14573                | R91813                | R51264                | 54             | ū                     | P60623   | W14568                |
| FeLV F6A provirus clo<br>Gene product of first | Rat type II collagen. | mot    | Survival motor neuron | Papillomavirus E2 bin | Ф      |         | CMV Colburn region po | Beta.    | ይ      | let      | Platelet glycoprotein | _      | Human bone morphogene |        | Guinea pig PH-30, 30 | Rape abscission/dehis | Streptococcus pneumon | Hepatitis E virus str | HEV strain protein en | MEKK5 protein. | Prod. of DNA of pMG07 |          | Streptococcus pneumon |
| 6.76e+01<br>6.76e+01                           | 6.76e+01              | . 7    |                       | 6.76e+01              |        |         |                       | 5.04e+01 | :      | 4.35e+01 | :.                    | : .    | <u>ب</u>              | W      | 3.75e+01             | ٠.                    | 3.75e+01              | ٠,                    | . 23                  | 'n             | . 23                  | 2.79e+01 | 3.23e+01              |

### ALIGNMENTS

| 8888888888888888                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               | 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0                                                                                                                                                                                                                                                                                                                                                               | RESULT ID W AC W DT 2 DE S                                                                                                                                                                                                        |
|------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|-----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|-----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| This sequence shows the central portion, including the c-terminus of the alpha-helix region and some of the proline-rich region, of pneumococcal surface protein A (PspA) of Streptococcus pneumoniae strain Bg9739. Comparison of the N-terminal and central regions (W14533-57 and W14562-91) of PspA polypeptides from different pneumococcal strains can be used to divide the strains into several families based on sequence homologies. PspA polypeptides, or fragments of them, can be used in vaccines to protect animals against 5. pneumoniae infection and hence for the prevention of diseases such as otitis media, meningitis, bacteraemia and pneumonia. The sequence of the 3' half of the PspA alpha-helical region and the immediate 5' tip of the coding sequence are likely to be the critical sequences for predicting PspA cross-reactions and vaccine Sequence 183 AA; | Streptococcus pneumoniae strain Bg9739.  WO970994-A1. 20-MAR-1997. 16-SEP-1996; U14819. 15-SEP-1995; US-529055. (UABR-) UAB RES FOUND. Briles DE, Brooks-Walter A, Crain MJ, Hollingshead S; MCDaniel LS, Swiatlo E, Tart R, Yother J; WFI; 97-202002/18. Streptococcus pneumoniae surface protein PspC and truncated PspA - used in vaccines for protecting animals against S.pneumoniae infection | M14570 standard; Protein; 183 AA. W14570; W14570; 28-OCT-1997 (first entry) Streptococcus pneumoniae PspA central region. PspA; pneumococcal surface protein; vaccine; otitis media; PspA; pneumococcal surface protein; vaccine; |

δõ g Query Match 9.1%; Score 101; DB 23; Length 183; Best Local Similarity 26.7%; Pred. No. 8.30e+00; Matches 20; Conservative 19; Mismatches 36; Indels 11 MTILQAPTPAPSTIPGPRRGSGPEIFTFDPLPEPAAAPAGRPSASRGHRKRSRRVLYPRV 70 

0,

Gaps

В

154

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 Matches
 Query Match
Best Local
 Sugar beet chitinase 4 and corresponding DNA - inhibits germination and growth of chitin-containing fungi and is used to produce genetically transformed plants
Claim 5; Page 164-168; 254pp; English.
A clone encoding the chitinase 1 gene was isolated from a sugar beet EMBL3 genomic library. The sequence encodes a protein having 439 amino acid residues. Transgenic plants having increased resistance to nematodes and chitin-containing plant pathogens, partic, fungi, can be produced using genetic constructs containing the chitinase 1 gene. The protein itself can be used in fungicidal
 Alpha 1b adrenergic receptor.
PCR; amplification; prostatic hypertrophy;
insulin resistance; hypertension; urinary r
erectile dysfunction; nasal congestion.
 T 3
R53072 standard;
R53072;
 07-APR-1992; DK0108.
08-APR-1991; DK-000616.
(DANI-) DANISCO AS.
Berglund L, Bojsen K, Mikkelsen
WPI; 92-366261/44.
 Homo sapiens W09408040-A.
 /label= proline_rich
/note= "possibly involved in anchoring
chitinase l protein to the cell wall
after modification of the prolines to
 Sugar beet chitinase SBC-1; fungicide; an
 21-SEP-1994 (first entry)
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 SBC-1; fungicide; anti-fungal agent; Beta vulgaris.cv monova.
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 Peptide
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Region 417..439
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 hevein_domain
47..178
 Similarity
25; Conser
 leader
 439 AA;
 9.0%;
llarity 30.1%;
Conservative
 (first entry)
 179..416
 Location/Qualifiers
 Protein;
 directs the
 Protein; 439
 85
 Score 100; DB 5; Le Pred. No. 9.67e+00; 13; Mismatches 44;
 protein
 B
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 JD,
 Nielsen KK;
 extensine
 retension;
 coronary heart disease;
 · inhibits
 Length 439
 Indels
 glaucoma;
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 Gaps
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 Query Match
Best Local
 Matches
 oligonuclotides, antibodies, etc - for determining ligand binding, drug screening and treatment of diseases associated with binding, drug screening and treatment of diseases associated with human alphal adrenergic receptors

Claim 43; Fig 2; 155pp; English.

In order to isolate a full length clone for the alpha 1 adrenergic receptor human cDNA libraries were screened by PCR with primers designed off the isolated genomic clones, from non conserved portions of the receptor gene. The PCR prod. was then used as a probe to isolate the full length alpha 1 adrenergic receptor gene. The gene can be used for screening for abnormalities associated with human alpha 1 adrenergic receptors. e.g. prostatic hypertrophy, coronary heart disease, insulin resistance, hypertension, urinary coronary heart disease, insulin resistance, hypertension, urinary
 retension, glaucoma, erectile dysfunction, Reynaud's syndrome, urinary incontinence and nasal conjestion.

See also R53071-3.
 Bard JA, Forray C, WPI; 94-135600/16.
 14-APR-1994.
24-SEP-1993; U09187
25-SEP-1992; US-952
 Sequence
 Alphal adrenergic receptor DNA,
 (SYNA-) SYNAPTIC PHARM CORP
 12 TILQAPTPAPSTIPGPRRGSGPEIFTFDPLPEPAAAPAGRPSASRG
 Similarity
 520 AA;
 8.8%;
ilarity 41.3%;
Conservative
 US-952798
 Weinshank
 Score 98; DB 9;
Pred. No. 1.31e+01
 9;
 RL;
 proteins, probes, antisense to - for determining ligand atment of diseases associated
 Mismatches
 15;
 Length 520
 Indels
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PRESULT PROCESS OF THE SECOND PROCESS OF THE
 cc hyperplasia which comprises administering a therapeutically effective amount of a compound which binds to a human alpha-1C CC adrenergic receptor with a binding affinity greater than ten-fold CC higher than the binding affinity with which the compound binds to a CC human alpha-1A adrenergic receptor or a human alpha-1B adrenergic receptor. The example concerns a protocol for the determination of CC transfecting the cloned cDNA or cloned genomic DNA or constructs CC contg. both genomic DNA and cDNA encoding human alpha-drenergic CC contg. both genomic DNA and cDNA encoding human alpha-adrenergic CC contg. both genomic DNA and cDNA encoding human alpha-adrenergic CC contg. both genomic DNA and cDNA encoding negion and 5' and 3' CC CC TRS were cloned into the BamHI and ClaI sites of the CC polylinker-modified eukaryotic expression vector pcrylinker-modified entire coding region and 5' and 3' UTRS CC CONTS or alpha-1B, the entire coding region and 5' and 3' UTRS CC CONTS or alpha-1C, the entire coding region and 5' and 3' UTRS CC CONTS or alpha-1C, the entire coding region and 5' and 3' UTRS CC CONTS or alpha-1C, the entire coding region and 5' and 3' UTRS CC CONTS or alpha-1C, the entire coding region and 5' and 3' CC CONTS or alpha-1C, the entire coding region and 5' and 3' CC CONTS or alpha-1C, the entire coding region and 5' and 3' CC CONTS or alpha-1C, the entire coding region and 5' and 3' CC CONTS or alpha-1C coding region and 5' and 3' CC CONTS or alpha-1C coding region and 5' and 3' CC CONTS or alpha-1C coding region and 5' and 3' CC CONTS or alpha-1C coding region and 5' and 3' CC CONTS or alpha-1C coding region and 5' and 3' CC CONTS or alpha-1C coding region and 5' and 3' CC CONTS or alpha-1C coding region and 5' and 3' CC CONTS or alpha-1C coding region and 5' and 3' CC CONTS or alpha-1C coding region and 5' and 3' CC CONTS or alpha-1C coding region and 5' and 3' CONTS or alpha-1C coding region and 5' and 3' CONTS or alpha-1C coding region and 5' and 3' CONTS or alpha-1C coding region and 5' and 3'
 Example; Page 46-51; 69pp; English. The inventors claim a method of treating
 Treating benign prostatic hyperplasia - with (
selectively to alphalC adrenergic receptor to
of prostatic tissue
 WPI;
 R52831 9
R52831;
 N-PSDB; Q62817.
 Branchek TA,
 26-MAY-1994.
12-NOV-1993; U10950.
13-NOV-1992; US-975867.
(SYNA-) SYNAPTIC PHARM
 10-NOV-1994 (first entry)
Sequence of human alpha 1
 Wetzel JM;
 WO9410989-A.
 Homo sapiens.
 Alpha 1B;
 94-183130/22.
 standard; Protein;
 adrenergic
 chiu G,
 receptor; antagonist;
 CORP
 Forray
 520
 B adrenergic receptor.
 ი,
 B
 Gluchowski
 neuroreceptor.
 cpds. which bind
inhibit contraction
 ú
 Hartig
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RESULT STANFORM OF Š
 PT Isolated DNA encoding a human N-methyl-D-aspartate receptor subunit - used as probes in the identification and isolation of PT subunit - used as probes in the identification and isolation of PT nucleic acids encoding related receptor subunits.

PS Claim 11; Page 99-104; 156pp; English.

CC 16 (NMDAR2C) gene clone NMDA21. This clone covers the a.a. 249-1040 of CC (RMDAR2C) gene clone NMDA21. This clone covers the a.a. 249-1040 of CC the complete NMDAR2C protein (079372) with the exception of a 17 a.a. CC deletion of a.a. 722-738 of the NMDAR2C sequence. The NMDA receptor contains two subunits: subunit R1 (079370) and subunit R2 selected from CC the subunits 2A (079375), 2B (079377), 2C and 2D (079378). The receptor forms part of a family of NMDA receptors which have cation selective companity and bind glutamate and NMDA. The NMDAR2C gene was obtained by corresponding to sequences in the rat NMDAR2C gene was obtained by corresponding to sequences in the rat NMDAR2A receptor DNA and using the resultant fragments as probes to screen a CDNA library derived from human hippocampal RNA. 4 basic clones were isolated: NMDA21 (079399), NMDA22 (079400), NMDA24 (079401) and NMDA26 (079402). The clones are thought to be splice variants of each other. Based on the sequence of the 4 clones, a series of variants (079403-7) of the NMDAR2C receptor were constructed. The expression of the genes allows the reconstruction of the NMDA CC planes are thought to be splice variants of each other. Based on the sequence of the 4 clones, a series of variants (079403-7) of the NMDAR2C receptor were constructed. The expression of the genes allows the reconstruction of the NMDA CC planes are thought to be paid to a series of variants (079403-7) of the NMDAR2C receptor were constructed. Sequence of the 4 clones, a series of variants (079403-7) of the NMDAR2C receptor were constructed. The compounds which be sequenced to the human NMDA receptor.
 g
 Query Match
Best Local S
Matches 1
 sequence betw W09424284-A. 27-OCT-1994.
 20-APR-1994; U04387.
20-APR-1993; US-052449.
(SALK) SALK INST BIOTECHNOLOGY IND ASSOC.
Daggett LP, Ellis SB, Liaw CW, Lu C;
WPI; 94-341863/42.
 06-JUL-1995 (first entry)
Human NMDAR2 receptor subunit clone NMDA21 protein.
N-methyl-D-aspartate; receptor; human; NMDA; cation-selective;
glutamate; hippocampus; rat; pcDNA1; NMDA receptor; antagonist
 Human NMDAR2 receptor subunit clone NMDAR2C-delta15-delta51 gene N-methyl-D-aspartate; receptor; human; NMDA; cation-selective; ciglutamate; hippocampus; rat; pcDNA1; NMDA receptor; antagonist.
20-APR-1994; U04387.
20-APR-1993; US-052449.
20-APR-1993; US-052449.
(SALK) SALK INST BIOTECHNOLOGY IND ASSOC Daggett LP, Ellis SB, Liaw CW, Lu C; WPI; 94-341863/42.
N-PSDB; Q79407.
 Misc_difference 716..717
/note= "17 a.a. deletion
between these residues"
 /note- "5 a.a. deletion of NMDAR2C a.a: sequence between these residues"
 Key Location/Qualifiers Misc_difference 591..592
 06-JUL-1995
 R66065 standard;
R66065;
 N-PSDB; Q79399
 Misc_difference 473..47
/note= "deletion of 17
 Homo sapiens.
 WO9424284-A.
 Homo sapiens.
 664 apppspcptprsgpspclptpdpppepsptgwgppdggra 703
:|:|| | | | | ::| : | | | | | | ::|:
18 TPAPSTIPGPRRGSGPEIFTFDPLPEPAAAPAGRPSASRG 57
 Similarity 42.5%, 17; Conservative
 (first entry)
 Location/Qualifiers
 Protein; 1214
 4 8
 residues"
 5 6
 of NMDAR2C
 Score
Pred.
11; M
 Ą
 NMDAR2C
 Mismatches 12;
 No.
 a.a. sequence
 DB 12;
1.78e+01;
 Length
 Indels
 0
 channel;
 channel;
 0
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QΥ
 PT Isolated DNA encoding a human N-methyl-D-aspartate receptor subunit - used as probes in the identification and isolation of PT nucleic acids encoding related receptor subunits.

PT nucleic acids encoding related receptor subunits.

PS Claim 11; Page 99-104; 156pp; English.

CC Caim 11; Page 99-104; 156pp; English.

CC CIMDAR2C) gene clone NMDAR2C-delta51. This clone covers the CC same sequence as the NMDAR2C sequence but contains deletions of a.a.

CC 591-5 and 722-38 of the NMDAR2C protein (R66035). A series of variants CC (Q79403-7) of the NMDAR2C receptor were constructed, by recombination, CC based on the sequence of the 4 basic clones: NMDA21 (Q79399), NMDA22 (Q79400), NMDA24 (Q79401) and NMDA26 (Q79402). The NMDA receptor CC contains two subunits: subunit R1 (Q79370) and subunit R2 selected from CC the subunits 2A (Q79375), 2B (Q79377), 2C and 2D (Q79378). The receptor CC channels and bind glutamate and NMDA. The expression of the genes allows the reconstruction of the NMDA receptors which have cation-selective cused to identify compounds which bind or are antagonistic to the human CC NMDA receptor.
 PT nucleic acids encoding related receptor subunits.

PT nucleic acids encoding related receptor subunits.

Claim 11; Page 99-104; 156pp; English.

The amino acid sequence of the novel N-methyl-D-aspartate (NMDA) receptor creating amino acid sequence of the movel N-methyl-D-aspartate (NMDA) receptor creating amino acid sequence of the novel NMDARZC sequence but contains a deletion of a.a.

This clone covers the creating amino acid sequence but contains a deletion of a.a.

The NMDARZC protein (R6035). A series of variants (079403-7) of the NMDARZC receptor were constructed, by recombination, based on the sequence of the 4 basic clones: NMDA21 (079399), NMDA22 (079400), NMDA24 (079401) and NMDA26 (079402). The NMDA receptor contains two subunits: subunit R1 (079370) and subunit R2 selected from the subunits 2A (079375), 2B (079377), 2C and 2D (079378). The receptor forms part of a family of NMDA receptors which have cation-selective channels and bind creconstruction of the NMDA receptor. The complete receptor can be used to identify compounds which bind or are antagonistic to the human NMDA
 Matches
 Query Match
Best Local
 20-APR-1993; US-052449.
(SALK) SALK INST BIOTECHNOLOGY IND ASSOC.
Daggett LP, Ellis SB, Liaw CW, Lu C;
WPI; 94-341863/42.
WPSI; 97-9405.
 27-OCT-1994.
20-APR-1994; 1
20-APR-1993; 1
 Ney
Misc_difference 721..722
/note= "17 a.a. deletion of NMDAR2C between these residues"
 Human NMDAR2 receptor subunit clone pCMV-26-ScaI-21-NotI-24 protein N-methyl-D-aspartate; receptor; human; NMDA; cation-selective; changlutamate; hippocampus; rat; pcDNAL; NMDA receptor; antagonist.
 Isolated DNA encoding a human N-methyl-D-aspartate recember subunit - used as probes in the identification and isolation
 06-JUL-1995
 R66063
 Sequence
 NMDA receptor
 WO9424284-A.
 Homo sapiens.
 R66063
 907 apppspcptprsgpspclptpdpppepsptgwgppdggra
 Local Similarity hes 17; Conser
 18
 TPAPSTIPGPRRGSGPEIFTFDPLPEPAAAPAGRPSASRG
 standard;
 1219
 1214 AA;
 Conservative
 A
 Protein;
 42.5%;
 1219
 Score 96; DB 12; L
Pred. No. 1.78e+01;
11; Mismatches 12;
 A
 a.a sequence
 946
 57
 Length 1214;
 Indels
 0;
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 Gaps
 0
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Query Match Best Local S Matches 1

Similarity 17; Conse

8.6%; larity 42.5%; Conservative

Score Pred.

No.

DB 12; 1

Length 1219;

0

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 Query Match
Best Local S
Matches 1
 Matches
 Query Match
Best Local
 W14569
16-SEP-1996; U14819.
15-SEP-1995; US-539055.
(UABR-) UAB RES FOUND.
Briles DE, Brooks-Walter A,
McDaniel LS, Swiatlo E, Tari
 Streptococcus pneumoniae PspA central region.
PspA; pneumococcal surface protein; vaccine; otitis media;
meningitis; bacteraemia; pneumonia.
Streptococcus pneumoniae strain Bg8743.
 /note= "unidentified amino acid" Misc_difference 186
 Disclosure, Page 81-83, 108pp; English.
Human alpha-1B adrenergic receptor DNA (see T03128) was cloned into the Ecol site of eukaryotic expression vector pCEXV-3. The resulting plasmid was co-transfected with pGCcos3neo into LM(tk-), CHO and NIH5T3 cells. Cell lines selectively expressing the recept (R85943) were used to screen cpds. for antagonist activity. Sequence 520 AA;
 Use of selective alpha 1C adrenergic receptor antagonists – for treating benign prostatic hyperplasia or inhibiting contraction
 04-APR-1995; U04203.
13-APR-1994; US-228932.
(SYNA-) SYNAPTIC PHARM CORP.
 Homo sapiens. w09528157-A1.
 W09709994-A1.
 Misc_difference 97
 Misc_difference 95
 Misc_difference
 Misc_difference
 W14569;
 Branchek TA, Chiu G,
 Alpha-1B adrenergic receptor; antagonist;
 R85943 standard,
R85943;
 /note= "unidentified amino acid"
 /note= "unidentified amino acid"
 /note= "
 28-OCT-1997 (first entry)
 prostate tissue
 N-PSDB; T03128
 Wetzel JM;
 benign prostate hyperplasia.
 /note= "unidentified
 12-FEB-1996
 452 allslpapeppgrrg-rhdsgp-lftfklltepes-pgtdggasng 494
 12 TILQAPTPAPSTIPGPRRGSGPEIFTFDPLPEPAAAPAGRPSASRG
 12
 Local
 TILQAPTPAPSTIPGPRRGSGPEIFTFDPLPEPAAAPAGRPSASRG
 95-373623/48.
 standard;
 h 8.8%;
Similarity 41.3%;
19; Conservative
 h 8.8%;
Similarity 41.3%;
19; Conservative
 unidentified amino acid"
 Location/Qualifiers
 Protein; 190
 Protein;
 entry)
 amino
 Forray CC,
 Tart
 520
 acid"
 Score 98; DB 14; Le
Pred. No. 1.31e+01;
9; Mismatches 15;
 Pred.
9;
 Score 98;
Pred. No.
 Crain MJ, R, Yothe:
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 No. 1.31e+01;
Mismatches 15;
 Yother
 Gluchowski C,
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 Length 520;
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 Example 6; Fig 13; 296pp; English.

Example 6; Fig 13; 296pp; English.

Control of the alpha-helix region and some of the proline-rich region, of pneumococcal surface protein A (PspA) of Streptococcus pneumoniae strain Bg9163. Comparison of the N-terminal and central regions (W14533-57 and W14562-91) of PspA polypeptides from different pneumococcal strains can be used to divide the strains into several families based on sequence homologies. PspA polypeptides, or fragments of them, can be used in vaccines to protect animals against S. pneumoniae infection and hence for the prevention of diseases such as otitis media, meningitis, bacteraemia and pneumonia. The sequence of the 3' half of the PspA alpha-helical region and the sequences for predicting PspA cross-reactions and vaccine
 Query Match
Best Local S
Matches 2
 Query Match
Best Local (
 Matches
LT 8
R66057
R66057;
 prevention (
 New density enhanced protein tyrosine phosphatase - used to develop prods. to modify transcription, translation and/or activity of tyrosine phosphatase(s).

Claim 4: Page 34-38: 51pp: English.
A cDNA clone was obtd. (see T06027) from a HeLa cell cDNA library that encoded a novel density-enhanced Type III receptor-like PTP, designated huDEP-1 (R85203). huDEP-1 is useful for the study of PTPs and for the development of therapeutic or prophylactic cpds. e.g. for
 09-NOV-1995.
03-MAY-1995; U05512.
03-MAY-1994; US-237940.
(COLD-) COLD SPRING HARBOR LAB.
 Oestman A, Tonks NK; WPI; 95-393079/50.
 sequence composition.
 N-PSDB; T06027
 Streptococcus pneumoniae surface protein PspC and truncated PspA used in vaccines for protecting animals against S.pneumoniae
 WO9530008-A1.
 Homo sapiens
 Density enhanced Type III receptor-like protein tyrosine phosphatase
 R85203 standard; Protein; 1337
 812 gitdppppdgspnitsvshnsvkvkfsgfeashgpikayavilttgeaghpsa
 huDEP-1
 huDEP-1
 115
 infection
 WPI; 97-202002/18.
 2-FEB-1996
 104
 16
 76 PVEEPNPAKR 85
 GVPAPLPPEDAPNAASLAPTPVSPVLEPFNLTSEP-SDYALDLSTFLQQHPAA
 paekpapapk
 APTPAPSTIPGPRRGSGPEIFTFDPLPEPAAAPAGRPSASRGHRKRSRRVLYPRVVRRQL 75
 Similarity
17; Conser
 h 8.7%;
Similarity 31.4%;
22; Conservative
 of abnormal or malignant 1337 AA;
 8.7%;
larity 32.1%;
Conservative
 Score 97; D
Pred. No. 1.
13; Mismatc
 Score 97; DB 23;
Pred. No. 1.53e+01;
15; Mismatches 31
 Mismatches
 cell growth
 DB 14;
1.53e+01;
 Length 1337;
 Length 190
 Indels
 155
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 Gaps
 Gaps
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standard; Protein;

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RESULT ACCORD RESULT THE SULT FOR SULT
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 risolated DNA encoding a human N-methyl-D-aspartate receptor subunit - used as probes in the identification and isolation of production in the production of a sequence of the involvence but contains a delection of a.a. 591-5 co fithe NMDAR2C sequence but contains a delection of a.a. 591-5 co fithe NMDAR2C protein (R66035). A series of variants (Q79403-7) of the NMDAR2C receptor were constructed, by recombination, based on the sequence of the 4 basic clones: NMDA21 (Q7939), NMDA22 (Q79400), NMDA24 (Q79401) and NMDA26 (Q79402). The NMDA receptor contains two subunits: subunit R1 (Q79370) and subunit R2 selected from the subunits 2A (Q79375), 2B (Q79377), 2C and 2D (Q79375). The receptor forms part of a camily of NMDA receptors which have cation-selective channels and bind CC reconstruction of the expression of the genes allows the used to
 Query Match
Best Local
 Matches
 27-OCT-1994;
20-APR-1994;
20-APR-1993;
 20-APR-1994; U04387.
20-APR-1993; US-052449.
(SALK) SALK INST BIOTECHNOLOGY:
Daggett LP, Ellis SB, Liaw CW,
WPI; 94-341865/42.
 Human NMDAR2 receptor subunit clone pCMV-26-ScaI-22 protein. N-methyl-D-aspartate; receptor; human; NMDA; cation-selective; channel; glutamate; hippocampus; rat; pcDNA1; NMDA receptor; antagonist.
 20-APR-1994; U04387.
20-APR-1993; US-052449.
(SALK) SALK INST BIOTECHNOLOGY IND ASSOC.
Daggett LP, Ellis SB, Liaw CW, Lu C;
WPI; 94-341863/42.
 Human N-methyl-D-aspartate receptor subunit 2C protein. N-methyl-D-aspartate; receptor; human; NMDA; cation-selective; channel; glutamate; hippocampus; rat; pcDNAl; NMDA receptor; antagonist.
 N-PSDB; Q79404.
 Misc_difference 591..592
/note- "5 a.a. deletion of NMDAR2C a.a. sequence between these residues"
 T 11
R66062 standard;
 Homo sapiens.
 Isolated DNA encoding a human N-methyl-D-aspartate receptor subunit - used as probes in the identification and isolati
 N-PSDB; Q79372.
 WO9424284-A.
 05-JUL-1995 (first entry)
 R66037;
 R66037 standard;
 Homo sapiens.
 06-JUL-1995 (first entry)
 R66062;
 nucleic acids
 924 apppspcptprsgpspclptpdpppepsptgwgppdggra 963
 identify compounds which bind or are antagonistic to the human
 18
 18 TPAPSTIPGPRRGSGPEIFTFDPLPEPAAAPAGRPSASRG
 TPAPSTIPGPRRGSGPEIFTFDPLPEPAAAPAGRPSASRG
 17;
 Similarity
 1231 AA;
 Conservative
 encoding
 Location/Qualifiers
 Protein;
 42.5%;
 related
 1231
 1236 AA
 Score
Pred.
11; M
 A
 IND ASSOC
 Mismatches
 No ;
 ш
 DB 12;
1.78e+01
 12;
 57
 Length 1231;
 isolation
 0;
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 Gaps
 NMDA
 0
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 PS Claim 11; Page 99-104; 155pp; English.

CThe amino acid sequence of the novel N-methyl-D-aspartate (NMDA) receptor CC (NMDAR2C). The NMDA receptor contains two subunits: subunit R1 CC (079370) and subunit R2 selected from the subunits 2A (079375), 2B CC (079377), 2C and 2D (079378). The receptor forms part of a family of CC NMDA receptors which have cation selective channels and bind glutamate and MNDA. The NMDAR2C gene was obtained by amplifying cDNA derived from human brain tissues with primers corresponding to sequences in the rat CN NMDAR2A receptor DNA and using the resultant fragments as probes to screen a cDNA library derived from human hippocampal RNA. 4 basic clones covere isolated: NMDA21 (07939), NMDA22 (079400), NMDA24 (079401) and MNDA26 (079402). The clones are thought to be splice variants of each other. Based on the sequence of the 4 clones, a series of variants contern. Based on the sequence of the 4 clones, a series of variants of the genes allows the reconstruction of the NMDA receptor. The complete creceptor can be used to identify compounds which bind or are antagonistic to the human NMDA receptor.
 PT Isolated DNA encoding a human N-methyl-D-aspartate receptor subunit - used as probes in the identification and isolation of production and isolation of production and isolation of production and isolation of production and isolation and isolation of production in the subunits.

Claim 11: Page 99-104: 156pp; English.

PS Claim 11: Page 99-104: 156pp; English.

CC The amino acid sequence of the novel N-methyl-D-aspartate (NMDA) receptor CC (NMDAR2C) gene clone NMDAR2C-delta15-I24. This clone covers the same cc sequence as the NMDAR2C sequence but contains a deletion of a.a. 591-5 (and an insertion of 8 a.a. between a.a. 721-2 of the NMDAR2C protein CC (R66035). A series of variants (079403-7) of the NMDAR2C receptor were constructed, by recombination, based on the sequence of the 4 basic (2010 of the Contain the Sequence of the 4 basic (2010 of the Series of variants (2079403), NMDA24 (2079401) and NMDA26 (2010 of the Series
 Query Match
Best Local :
 Matches
 27-OCT-1994.
20-APR-1994; U04387.
20-APR-1993; US-052449.
20-APR-1993; US-052449.
(SALK) SALK INST BIOTECHNOLOGY IND ASSOC Daggett LP, Ellis SB, Liaw CW, Lu C; WPI; 94-341863/42.
WPI: 94-341863/42.
WPSDB: Q79406.
 Human NMDAR2 receptor subunit clone NMDAR2C-delta15-124 protein. N-methyl-D-aspartate; receptor; human; NMDA; cation-selective; channel; glutamate; hippocampus; rat; pcDNA1; NMDA receptor; antagonist.
 /note= "5 a.a deletion o
between these residues "
Misc_difference 717...723
 R66064;
06-JUL-1995
 Location/Qualifiers
Misc_difference 591..592
/note= "R ~ -
 R66064 standard; Protein; 1239
 The complete receptor can antagonistic to the human sequence 1239 AA;
 WO9424284-A.
 /note=
 Homo sapiens
 929 apppspcptprsgpspc1ptpdpppepsptgwgppdggra 968
 18 TPAPSTIPGPRRGSGPEIFTFDPLPEPAAAPAGRPSASRG
 "8 a.a. insertion"
 h 8.6%;
Similarity 42.5%;
17; Conservative
 (first entry)
 of NMDAR2C a.a. sequence
 NMDA receptor.
 Score 96; D
Pred. No. 1.
11; Mismatc
 Ş
 Mismatches
 DB 14,
1.78e+01;
1.71
 12;
 Length 1236;
 0
 0
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Query Match Best Local

Matches

Similarity 17; Conser

Conservative 42.5%;

Score 96; DB 12; Pred. No. 1.78e+01; 11; Mismatches 12

Length 1239;

Indels

0

Gaps

S B

932 apppspcptprsgpspclptpdpppepsptgwgppdggra 971

18 TPAPSTIPGPRRGSGPEIFTFDPLPEPAAAPAGRPSASRG

57

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 subunit used as probes in the identification and isolation of nucleic acids encoding related receptor subunits.

PS Claim 11; Page 99-104: 156pp: English.

CT (NMDAR2C) gene clone pCHV-26-ScaI-24. This clone covers the same sequence as the NMDAR2C sequence and contains an insertion of 8 a.a. 72-8 of the NMDAR2C protein (R66035). A series of variants between a.a. 72-8 of the NMDAR2C protein (R66035). A series of variants (079403-7) of the NMDAR2C receptor were constructed, by recombination, based on the sequence of the 4 basic clones: NMDA21 (079399), NMDA22 (079400), NMDA24 (079401) and NMDA26 (079402). The NMDA receptor contains two subunits: subunit R1 (079370) and subunit R2 selected from the subunits 2A (079375), 2B (079377) and 2D (079378). The receptor the subunits 2A (079375), 2B (079377). 2C and 2D (079378). The receptor channels and bind glutamate and NMDA. The expression of the genes allows the reconstruction of the NMDA receptor. The complete receptor can be used to identify compounds which bind or are antagonistic to the human species 1244 AA:
 Query Match
Best Local S
Matches 1
 Cleavage_site 182..183
Misc_difference 3
/label= kinase c phosphorylation site
Misc_difference 42
/label= kinase c phosphorylation site
 R59841 standard; Protein; 198 R59841;
 20-APR-1994; U04387.
20-APR-1993; US-052449.
(SALK) SALK INST BIOTECHNOLOGY IND ASSOC
Daggett LP. Ellis SB, Liaw CW, Lu C;
 Misc_difference 722..728
/note= "8 amino > -: 3
 06-JUL-1995 (first entry)
Human NMDAR2 receptor subunit clone pCMV-26-ScaI-24 protein.
N-methyl-D-aspartate; receptor; human; NMDA; cation-selectiv
glutamate; hippocampus; rat; pcDNA1; NMDA receptor; antagoni
 Misc_difference 43
 ApoE4L protease:
ApoE4L; protease; enzyme; Alzheimer disease; diagnostic; therapeutic
 Isolated DNA encoding a human N-methyl-D-aspartate receptor subunit - used as probes in the identification and isolation
 WPI; 94-341863/42.
N-PSDB; Q79403.
 r 14
R66061 standard; Protein; 1244 AA.
 Cleavage_site
/label=
 Homo sapiens
 26-JAN-1995
 WO9424284-A.
27-OCT-1994.
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 Local Similarity hes 17; Conser
 18 TPAPSTIPGPRRGSGPEIFTFDPLPEPAAAPAGRPSASRG 57
kinase c phosphorylation site
 1244 AA;
 8.6%;
llarity 42.5%;
Conservative
 4 homology
e 43..44
e 182..183
 (first entry)
 89..104
 Location/Qualifiers
 Score 96; DB 12;
Pred. No. 1.78e+01
11; Mismatches 1;
 B
 NMDA receptor; antagonist.
 NMDA; cation-selective; channel;
 12;
 Length 1244;
 Indels
 0
 Gaps
 0
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Search completed: Fri Apr

17 13:41:26 1998

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3

Job time : 24 secs

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Best Local
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 Claim 22; Page 39-40; 72pp; English.

Apocsi is a protease catalyzing the formation of the abnormal beta/A4

variant of beta-amyloid protein, and is used to develop an inhibitor

for the diagnosis and teatment of Alzheimer disease, Downs syndrome,

Parkinson disease, schizophrenia, hyperlipoproteinemia or
 (PRED/) PREDDIE R E.
Bergmann JE, Preddie RE;
 /label= kinase c phosphorylation site
Misc_difference 87
/label= kinase c phosphorylation site
Misc_difference 112
 New proteinase esterase-like proteins - used to develop prods for the diagnosis and treatment of Alzheimer's disease and related diseases
 Bergmann JE, Pred
WPI, 94-234212/28.
 WO9413798-A.
 /label= kinase c phosphorylation
Misc_difference 129
 /label - kinase c phosphorylation Misc_difference 129
 Misc_difference 54
 cardiovascular disease.
 P-PSDB; Q69099.
 04-MAR-1993;
 16-DEC-1992;
 'label | kinase c phosphorylation
 40
 73
 | pareptvaartrpcstrgpr-rsrmalrprsapsrap 108
 PLPEPAAAPAGRPSASRGHRKRSRRVLYPRVVRRQLP
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Similarity 43.2%;
16; Conservative
 198 AA;
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US-291401.
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Pred. No.
5; Misma
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atches 15;
 DB 10;
 Length 198
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| ***                                                          | (TM) |

Release 3.0.4A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1997 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

Run on: MPsrch\_pp protein - protein database search, using Smith-Waterman algorithm Fri Apr 17 13:40:06 1998; MasPar time 10.54 Seconds 633.960 Million cell updates/sec

Tabular output not generated.

Title:

Sequence: Description: Perfect Score: >US-08-799-910-10 (1-156) from US08799910.pep 1114 1 MCHSRSCHPTMTILQAPTPA.....EPSDYALDLSTFLQQHPAAF 156

Scoring table: PAM 150 Gap 11

Searched: 195121 segs, 42852602 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

pir55 l:pir1 2:pir2 3:pir3 4:pir4

Statistics:

Database:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Mean 36.831; Variance 125.421; scale 0.294

## SUMMARIES

Result

| esult<br>No. | Score | Query<br>Match | Length | В | ID         | Description | dī | 10  | 5  |       | Pred. No. |
|--------------|-------|----------------|--------|---|------------|-------------|----|-----|----|-------|-----------|
| 1            | 1111  | 99             | 156    | 2 | JC5537     | This        | is | ω . | B  | line. | 8.18e-119 |
| 2            | 752   | 67.5           | 153    | N | S33363     | This        | ŝ  | מ   | 멆  | line. | .10e-     |
| w            | 117   | 10             | 474    | N | S15921     | This        | ĺs | Ø   | B  | line. | . 63      |
| 4            | 114   | 10             | 351    | Ν | B34768     | This        | żs | ω   | DE | line. |           |
| u            | 110   | 9              | 228    | N | S53504     | This        | żs | Ø   | Œ  | line. | -         |
| σ            | 109   | 9              | 1729   | N | MSETQEQEAS | This        | is | Ø   | DE | line. | 8.78e-01  |
| 7            | 102   | Q              | 753    | N | JQ0532     | This        | is | ω   | DE | line. |           |
| 80           | 103   | 9              | 913    | N | S20590     | This        | İs | മ   | B  | line. | .0        |
| 9            | 102   | 9              | 1106   | N | JQ0405     | This        | İs | Ø   | Е  | line. |           |
| 10           | 103   | 9              | 1206   | ν | S24407     | This        | ż  | മ   | H  | line. |           |
| 11           | 103   | 9              | 1468   | N | S11515     | This        | ŝ  | Ø   | B  | line. | 3.00e+00  |
| 12           | 101   | 9              | 268    | 2 | в39429     | This        | į  | Ø   | DE | line. | 4.49e+00  |
| 13           | 101   | 9              | 417    | N | E30341     | This        | s, | Ø   | B  | line. | 4.49e+00  |
| 14           | 101   | 9              | 816    | N | F31277     | This        | ż  | ໝ   | DE | line. | 4.49e+00  |
| 15           | 100   | 9              | 333    | N | S61849     | This        | ž  | Ø   | DE | line. | ٠.        |
| 16           | 100   | 9              | 439    | N | S51939     | This        | ŝ  | Ø   | DE | line. | . 49      |
| 17           | 100   | 9              | 1492   | N | A40333     | This        | S, | D   | DΕ | line. | 5.49e+00  |
| 18           | 99    | 89             | 272    | N | A47021     | This        | ş  | Ø   | DE | line. | . 7 (     |
| 19           | 98    | œ              | 272    | N | S28013     | This        | is | Ø   | Œ  | line. | 8.17e+00  |
| 20           | 98    | œ              | 351    | N | S50754     | This        | s, | Ø   | DE | line. | <u>-</u>  |
| 21           | 98    | 8              | 390    | Н | QQBE77     | This        | ş  | D   | Œ  | line. | <u>.</u>  |
| 22           | 98    | 8              | 475    | N | v          | This        | ż  | þ   | DE | line. | 1         |
| 23           | 98    | 8              | 516    | N | JC2332     | This        | is | ည   | DE | line. | 8.17e+00  |
|              |       |                |        |   |            |             |    |     |    |       |           |

|                                                                                                  | %00000HVHVHVHVH                                                                                                                                                                                                                                                      | 0 11 0 11 0 11                                                                                                                                                                                                                          | WHX & X D X D X D X D X                                                                                                                                                                                                                                                                       |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   |
|--------------------------------------------------------------------------------------------------|----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|-----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|-----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|-------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| Query Match 67.5%; Score 752; DB 2; Length 153; Best Local Similarity 70.6%; Pred. No. 1.10e-74; | RESULT 2 ID S33363 STANDARD; PRT; 153 AA.  XX XX XX DT 01-JAN-1900 XX XX This is a DE line. XX XX C: Genetics: C: Genetics: C: A: Introns: 70/3 CC C: Keywords: transmembrane protein CC C: Keywords: transmembrane protein SQ SEQUENCE 153 AA; 16875 MW; 122478 CN; | Query Match  99.7%; Score 1111; DB 2; Length 156;  Best Local Similarity 99.4%; Pred. No. 8.18e-119;  Matches 155; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  Db 1 MCHSRSCHPTMTILQAPTPAPSTIPGPRRGSGPEITTDPLPEPAAAPAGRPSGSRGHRK 60 | RESULT 1 ID JC5537 STANDARD; PRT; 156 AA.  XX AC XXXXXX AC XXXXXX  XX O1-JAN-1900 This is a DE line.  XX XX DE This is a DE line.  XX XX CC A; Experimental source: monocyte CC A; Note: the authors translated the codon CCG for residue 106 as Arg SO SEQUENCE 156 AA; 16914 MW; 127043 CN; | 24 98 8.8 517 2 A45121 This is a DE line. 8.17e+00 25 98 8.8 975 2 S33121 This is a DE line. 8.17e+00 26 98 8.8 1486 2 B40333 This is a DE line. 8.17e+00 27 97 8.7 1239 1 QQBE10 This is a DE line. 9.95e+00 28 97 8.7 1337 1 I38670 This is a DE line. 9.95e+00 30 96 8.6 245 1 W4WL5 This is a DE line. 9.95e+00 31 96 8.6 245 1 W4WL5 This is a DE line. 1.21e+01 32 96 8.6 245 1 W4WLB This is a DE line. 1.21e+01 33 95 8.5 316 2 G20424 This is a DE line. 1.21e+01 36 95 8.5 316 2 S55611 This is a DE line. 1.47e+01 37 95 8.5 37 2 A48018 This is a DE line. 1.47e+01 38 95 8.5 37 2 A48018 This is a DE line. 1.47e+01 39 95 8.5 449 2 S16748 This is a DE line. 1.47e+01 40 95 8.5 386 2 S21061 This is a DE line. 1.47e+01 41 95 8.5 3866 2 B48205 This is a DE line. 1.47e+01 42 95 8.5 3869 2 S27200 This is a DE line. 1.47e+01 43 94 8.4 389 2 S27200 This is a DE line. 1.47e+01 45 94 8.4 473 2 S50755 This is a DE line. 1.79e+01 47 94 8.4 473 2 S50755 This is a DE line. 1.79e+01 48 94 8.4 473 2 S50755 This is a DE line. 1.79e+01 48 94 8.4 473 2 S50755 This is a DE line. 1.79e+01 48 94 8.4 473 2 S50755 This is a DE line. 1.79e+01 |

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 SEQUENCE
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 A;Molecule type: DNA
A;Residues: 207-474 <NEW>
A;Cross references: EMBL:X14717
 submitted to the EMBL Data Library, March 1989
A;Reference number: S06686
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 R; Neumann, H.; Zillig, W.
Nucleic Acids Res. 18, 2171, 1990
A;Tille: Nucleotide sequence of the viral
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A; Start cod
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 121
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 69 RVVRRQLPVEEPNPAKRLLFLLLTIVFCQILMAEEGVPAPLPPEDAPNAASLAPTPVS 126
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 PTMTILQAPTPAPSTIPGPRRGSGPEIFTFDPLPEPAAAPAGRPSASRGHRKRSRRVLYP
 AP--TPVS--PVLEPFNLTSEPSDYALDLSTFL
 EPISAPITAPPVLEPLNLTSESSDYALDLKAFL 153
 RSRRVLYPRVVRRQLPTEEPNIAKRVLFLLFAIIFCQILMAEEGVSQPLAPEDATSAVTP 120
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23.7%;
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 PRT;
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 R;Abrahams, S.; Hayes, C.M.;
Plant Mol. Biol. 27, 513-528,
A:Title: Expression patterns
A;Reference number: $53504
A;Accession: $53504
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A; Residues: 1-228 < AB
 C;Species: Medicago sativa (alfalfa)
C;Date: 15-Jul-1995 #sequence_revision
 extensin-like protein S3 - alfalfa
 >P1;S53504
 236
 RiFraser, K.M.; Hill, D.F.; Mercer, A.A.; Robinson, Virology 176, 379-389, 1990
A:Title: Sequence analysis of the inverted terminal A:Reference number: A34768; MUID:90266454
A:Accession: B34768
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 15 QAPTPAPSTIPGPRRGSGPEIFTFDPLPE-PAAAPAGRPSASRGHRKRSRRVLYPRV-VR
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 PPTPPANTPPTTPQASPPPVQS-SPPPVQSSPPPVQSSPPPAQSTPPPVQSSPPPVSAPP 94
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 of: b34768
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larity 32.9%;
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 C.M.; Watson, J.M.
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 Score 110; DB 2; L
Pred. No. 7.13e-01;
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 This is a DE line.
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 01-JAN-1900
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A;Residues: 1-753 <DIN>
A;Experimental source: strain Jervis Bay isolate
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 328
 271 LPRPGNRPGVLPGPKVRGA-PSS-NL-PLPTPQAPPRARERLQRSLHLHASRQNAPRLRP 327
 130 EPFNLTSEPSD 140
 892 FEFDLSGSSDQ 902
 >P1;S20590
exo-alpha-sialidase (EC
 y Match 9.2%;
Local Similarity 32.9%;
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 72 RR-QLPVEEPNPAKRLLFLLLTIVFCQILMAEEGVPAPLP-PEDAPNAASLAPTPVSPVL 129
 14 LQAPTPAPSTIPGPR-RGSGPEIFTFDPLPEPAAAPAGRPSASRGHRKRSRRVLYPRVVR 72
 TOIG of: s20590
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 ILQAPTPAPSTIPGPRRGSGPEIFTFDPLPEPAAAPAGR-PSASRGHRKRSRRVLYPRVV 71
 RQLPVEEPNPAKR 85
 RRLR-SDPIQQTR 339
 Similarity
31; Conser
 1729 AA; 194986 MW; 14801419
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 Conservative
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23.7%;
 check:
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 3.2.1.18) -
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Pred. No. 8.78e-01;
30; Mismatches 65;
 Score 102; DB 2;
Pred. No. 3.67e+00;
14; Mismatches 30
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 RESULT 10
ID S24407
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C;Species: Mus musculus (house mouse)
C;Date: 19-Feb-1994 #sequence_revision
 A; Reference number: A; Accession: S20590
 A; Accession: JQ0405
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 76 PVEEPNP
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 20;
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 STANDARD;
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 880
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A; Residues: 1-1106 <SHI>
A; Cross-references: EMBL:X15867
A; Onte: all the codons between two in-frame stop codons are translated; the A; Note: the gene encoding this protein overlaps uvrA gene
SEQUENCE 1106 AA; 119484 MW; 4705861 CN;
 C;Species: Actinomyces viscosus
C;Date: 22-Nov-1993 #sequence_revision 01-Dec-1995 #text_change
C;Accession: S20590
R;Henningsen, M.; Roggentin, P.; Schauer, R.
Biol. Chem. Hoppe-Seyler 372, 1065-1072, 1991
Biol. Chem. Hoppe-Seyler 372, 1065-1072, 1991
A;Title: Cloning, sequencing and expression of the sialidase gen
A;Reference number: S20590; MUID:92162190
 A;Cross-references: EMBL:X62276; NID:g39254; PID:g39255
C;Keywords: glycosidase; hydrolase
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 569 PGPAGVPAGRRPRVPQPRAAGRHPLRRRGPA-HPPGHTDRLRAGRRPLRDRRAVHRPAPA 627
 816 SPAPSRNAAPTPKPGMEPDEID-RPSDGTMAQPTGAP-ARRVPRRRRRRRPAAGCLARDQ 873
 16 APTPAPSTIPGPRRGSGPEIFTFDPLPEPAAAPAGRPSASRGHRKRSRRVLYPRVVRRQL 75
 PAPSTIPGPRRGSGPEIFTFDPLPEPAAAPAGRPSASRGHRKRSRRVLYPR-VVRRQLPV
 h 9.2%;
Similarity 29.9%;
20; Conservative
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llarity 29.9%;
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 Score 102; DB 2;
Pred. No. 3.67e+00;
16; Mismatches 29
 Score 103; DB 2; L
Pred. No. 3.00e+00;
14; Mismatches 31;
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CC 701G
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A; Residues: 1-1206 <AAC>
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 SEQUENCE
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C;Date: 22-Jan-1994 #sequence_revision
C;Accession: S11515
R;Woychik, R.P.; Maas, R.L.; Zeller, R.
Nature 346, 850-853, 1990
 C;Accession: S24407
R;Jackson-Grusby, L.; Kuo, A.; Leder, P.
Genes Dev. 6, 29-37, 1992
A;Title: A variant limb deformity transcript
A;Reference number: S24407; MUID:92112033
A;Accession: S24407
 A;MOlecule type: mRNA
A;Residues: 1-1468 <WOY>
A;Residues: 1-1468 <WOY>
A;Cross-references: EMBL:X53599; NID:g52877;
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 942 VLALPNSGGPPP-PPPPPPPPPPPGLAPPP-PPGL-SFGLSSSSSQYP
 A; Accession: S11515
 A; Title: 'Formins': proteins deduced from the alternative transcripts of the limb A; Reference number: S11515 \,
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RESULT 14
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 C;Accession. Paramentier, M.; Lefort, A., Perone, R;Libert, F.; Parmentier, M.; Lefort, A., Perone, Science 244, 569-572, 1989
A;Title: Selective amplification and cloning A;Title: A30341; MUID:89242119
 R:Geever, R.F.; Huiet, L.; Baum, J.A.; Tyler, B.M.; J. Mol. Biol. 20, 15-34, 1989 A;Title: DNA sequence, organization and regulation A;Reference number: S04250; MUID:89293848 A;Accession: S04256
 N;Alternate names: QA activator
C;Species: Neurospora crassa
C;Date: 26-Apr-1989 #sequence_revision 26-Apr-1989 #text_change 12-Sep-1997
C;Accession: S04256; F31277
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A; Residues: 1-417 <LI5>
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 C; Accession: E30341
 >F1; E30341
 142 CAQTVVSLAAAAQPTPPTSPEPPRGSPGPSLAP-GPVREKGAGKRGPDRGSPEYRQRRER 200
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 A; Cross-references:
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 7
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Similarity 43.68;
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 Query Match 9.1%;
Best Local Similarity 33.3%;
Matches 16; Conservative
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A;Gene: hrpV
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 01-JAN-1900
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A;Residues: 1-333 <VAND
A;Cross-references: EMBL:Z14056; NID:g550397; PID:g550401
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, September
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 408 VVRTQLPPDDDRPRPRMRALLVACFIVDTIVSMRHNVPAHLKPDDIAD 455
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 70 VVRRQLPVEEPNPAKRLLFLLLTIVFCQILMA-EEGVPAPLPPEDAPN 116
 RITGPSSAIY-TLPDPATTPAQPAAATPNTHRRRPRQ-LHEREIEHE 47
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 Score 100; DB 2;
Pred. No. 5.49e+00;
14; Mismatches 14
 333 AA.
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| •   | PRG1 PROTEIN (DIF-2 PR 8.46e-174 HOMOLOGUE OF RETROVIRA 3.65e-02 CELL WALL PROTEIN PREC 3.65e-02 GENOME, PARTIAL SEQUEN 6.41e-02 PROLINE RICH PROTEIN P 6.41e-02 PROLINE RICH PROTEIN P 6.41e-02 MYROSINASE-BINDING PRO 1.12e-01 SIMILAR TO CUTICULAR C 5.74e-01 VACCINIA VIRUS GENE F1 5.74e-01 MCACINIA VIRUS GENE F1 5.74e-01 SIALIDASE (EC 3.2.1.18 4.39e-01 ENDOGLUCANASE A (EC 3.2.1.8 4.39e-01 CUT-LIKE 2 (CUX-2). 4.39e-01 PUTATIVE PROLINE-RICH 9.79e-01 HRPV. 79e-01 CTD-BINDING SR-LIKE PR 9.79e-01 CTD-BINDING SR-LIKE PR 9.79e-01 CTD-BINDING SR-LIKE PR 9.79e-01 | PRG1 PROP<br>HOMOLOGUE<br>PREDICTEE<br>CELL WALL<br>U136.<br>GENOME, E<br>GENOME, E<br>PROLINE H<br>MYROSINAL<br>SIMILAR 7<br>ARTICULIN<br>VACCINIA<br>MC018L<br>ENDOGLUGA<br>CUT - LIKE<br>PUTATIVE<br>CUT- LIKE<br>PUTATIVE<br>CTD BIND:<br>ALPHA-1 | Q953091<br>P985306<br>P78977<br>Q658553<br>Q84630<br>Q96343558<br>Q96343558<br>Q963453<br>Q9634171<br>Q963111<br>P70629164<br>Q59164<br>Q59164<br>Q59164<br>Q59164<br>Q59164<br>Q5272194<br>Q5272194<br>Q53627<br>Q53627 | 156 1<br>351 9<br>285 1<br>3247 1<br>3247 1<br>3247 1<br>3248 8<br>558 3<br>418 8<br>418 3<br>418 1<br>680 11<br>680 11<br>1426 10<br>1426 8<br>333 9<br>448 10<br>1491 12 | 100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00 | 1114<br>1112<br>1112<br>1112<br>1110<br>1110<br>1100<br>1002<br>1002<br>1003<br>1003 | 1<br>3<br>3<br>5<br>5<br>5<br>6<br>7<br>7<br>7<br>1<br>1<br>1<br>1<br>1<br>1<br>1<br>1<br>1<br>1<br>1<br>1<br>1<br>1<br>1<br>1 |
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|     | ription Pred. No                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               | S                                                                                                                                                                                                                                                     | : 5                                                                                                                                                                                                                      | 1 10                                                                                                                                                                       | 양각                                                                                     | Score                                                                                | Result                                                                                                                         |
| ·   | of the result being printed, core distribution.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | s predice e score total s                                                                                                                                                                                                                             | of results plants of the                                                                                                                                                                                                 | number<br>n or eq<br>analys                                                                                                                                                | eater tha                                                                              | red. No<br>core gr                                                                   | ט פרט<br>ראי<br>טרט                                                                                                            |
|     | ertebrate<br>hage 8:sp_<br>sp_virus 1                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          | 3:sp_ir<br>e 7:sp_<br>dent 11                                                                                                                                                                                                                         | :sp_huma p_organe a 10:sp_ sified                                                                                                                                                                                        | p_ung                                                                                                                                                                      | 13:15:1                                                                                |                                                                                      | ataba                                                                                                                          |
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| • a |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | residues                                                                                                                                                                                                                                              | 2109429                                                                                                                                                                                                                  | S seqs, 4                                                                                                                                                                  | Gap 1                                                                                  | Q: .                                                                                 | Searche                                                                                                                        |
|     | EPSDYALDLSTFLQQHPAAF 156                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | 0.pep                                                                                                                                                                                                                                                 | -10<br>S08799910<br>ILQAPTPA.                                                                                                                                                                                            | S-08-799-910-10<br>-156) from US08799910<br>14<br>MCHSRSCHPTMTILQAPTPA.                                                                                                    | P 110                                                                                  | con:                                                                                 | . 455<br>                                                                                                                      |
|     | ar time 12.21 Seconds<br>123 Million cell updates/sec                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          | МаяР<br>538.                                                                                                                                                                                                                                          | 39:01 19                                                                                                                                                                                                                 | Apr 17 13: enerated.                                                                                                                                                       | Fri A                                                                                  | output                                                                               | Run on:<br>Fabular                                                                                                             |
| ·   | ting R<br>dinbur<br>lecula                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | , Biocom<br>rsity of<br>Oxford                                                                                                                                                                                                                        | Collin<br>7 Univ<br>ights b                                                                                                                                                                                              | 4A John F.<br>() 1993-199<br>() Induction r<br>() protein da                                                                                                               | se 3.0.<br>lght (c<br>bist                                                             | Releas<br>Copyri                                                                     | √Psrch_                                                                                                                        |
|     |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |                                                                                                                                                                                                                                                       |                                                                                                                                                                                                                          |                                                                                                                                                                            | *                                                                                      |                                                                                      | * * * * * * * * * * * * * * * * * * * *                                                                                        |

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| 94       | 94        | 94                 | 94       | 95                  | 95                     | 95                   | 95                     | 95           | 95                     | 95       | 96                     | 96       | 96      | 96                 | 96                     | 97       | 97       | 97                     | 97                      | 97             | 86                     | 98             | 99          | 99                |
|          | 8.4       | 8.4                | 8.4      | 8.5                 | 8<br>5                 | æ<br>.5              |                        | &<br>5       | 8<br>.5                | 8.5      | 8.6                    | 8<br>6   | 8.6     | 8<br>6             | 8.6                    | 8.7      | 8.7      | 8.7                    | 8.7                     | 8.7            | 8                      | 8.8            | 8.9         | 8                 |
| 581      | 517       | 473                | 165      | 1525                | 732                    | 665                  | 556                    | 533          | 336                    | 238      | 1236                   | 605      | 400     | 381                | 356                    | 5262     | 4957     | 1337                   | 496                     | 224            | 1486                   | 351            | 642         | 556               |
| w        | 9         | œ                  |          |                     |                        |                      |                        |              |                        |          |                        |          |         |                    |                        |          |          |                        |                         | 4              | 12                     | œ              | ω           | ď                 |
| Q20517   | Q51619    | Q39620             | Q39352   | Q21920              | Q13032                 | Q48373               | 015530                 | P93766       | Q66620                 | Q41883   | 015398                 | 015297   | 013107  | 015171             | 006979                 | 014686   | 014687   | Q15255                 | Q98457                  | 019031         | Q91717                 | Q39492         | 023831      | Q46043            |
| F47B8.5. | MOB3 ORF. | (VSP-3) PRECURSOR. | OLEOSIN. | R11A8.7 (FRAGMENT). | GABA/NORADRENALINE TRA | CHITINASE PRECURSOR. | 3-PHOSPHOINOSITIDE DEP | MLO PROTEIN. | CAPSID SCAFFOLD PROTEI | ZEIN.    | N-METHYL-D-ASPARTATE R | WIP1.    | BMP4.   | FORK HEAD PROTEIN. | HYPOTHETICAL 40.2 KD P | ALR.     | ALR.     | PROTEIN-TYROSINE PHOSP | GENOME, PARTIAL SEQUEN. | BACTINECIN 11. | ALPHA-1 TYPE II COLLAG | WP6 PRECURSOR. | (FRAGMENT). | BETA GLUCOSTUASE. |
| 4.67e+00 | 4.67e+00  | 4.67e+00           | 4.67e+00 | 3.61e+00            | 3.61e+00               | 3.61e+00             | 3.61e+00               | 3.61e+00     | 3.61e+00               | 3.61e+00 | 2.79e+00               | 2.79e+00 | 2.79e+0 | 2.79e+00           | 2.79e+00               | 2.15e+00 | 2.15e+00 | 2.15e+00               | 2.15e+00                | 2.15e+00       | 1.66e+00               | 1.66e+00       | 1.28e+00    | 1.20e+00          |

## ALIGNMENTS

| Qy<br>Db                                         | Oy Db                                                                   | Оу                                                                    | Qu<br>Be                                                                                                                                                          |                                            |                        | R A                             | 7 K      | R | RL                         | RA 7          | 0 X | P. P.                                                 | RA | ŖP                 | RN  | റ്റ | ဂ္ဂ       | SO:                  | ล เ      |             |                    |           |                                  | RESULT   |            |
|--------------------------------------------------|-------------------------------------------------------------------------|-----------------------------------------------------------------------|-------------------------------------------------------------------------------------------------------------------------------------------------------------------|--------------------------------------------|------------------------|---------------------------------|----------|---|----------------------------|---------------|-----|-------------------------------------------------------|----|--------------------|-----|-----|-----------|----------------------|----------|-------------|--------------------|-----------|----------------------------------|----------|------------|
| 121 APTPVSPVLEPFNLTSEPSDYALDLSTFLQOHPAAF 156<br> | 61 RSRRVLYPRVVRRQLPVEEDNPAKRLLFLLLTIVFCQILMAEEGVPAPLPPEDAPNAASL 120<br> | 1 MCHSRSCHPTMTILQAPTPAPSTIPGPRRGSGPEIFTEDPLPEPAAAPAGRPSASRGHRK 60<br> | Query Match 100.0%; Score 1114; DB 2; Length 156; Best Local Similarity 100.0%; Pred. No. 8.46e-174; Matches 156; Conservative 0; Mismatches 0; Indels 0; Gaps 0; | SEQUENCE 156 AA; 16928 MW; 46013510 CRC32; | EMBL: Y14551; E333102; | CANCER RES. 56:1498-1502(1996). | ROM N.A. |   | BIOPHYS. RES. COMMUN. 235: | C., ASLANIDIS |     | SUBMITTED (MAR-1996) TO EMBL/GENBANK/DDBJ DATA BANKS. |    | SEQUENCE FROM N.A. | [1] |     | RYOTA; MI | HOMO SAPIENS (HUMAN) | OR DIF-2 | (TREMBEREE: | CHREMBEREE OF TROP | 02, CREAT | Q92691 PRELIMINARY; PRT; 156 AA. | <b>—</b> | ALLONDENIO |

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LAST ANNOTATION UPDAT

UPDATE)

Score 112; DB 1; L. Pred. No. 3.65e-02; 29; Mismatches 70;

Length 285

Indels

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Gaps

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01-MAY-1997 (TREMBLREL. (
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 TYAGI J.S.;
SUBMITTED (FEB-1996) TO EMBL/GENBANK/DDBJ DATA BANKS.
EMBL; X63508; E282228; -.
 VERMA A.,
INDIAN J.
 SEQUENCE FROM N.A.

MEDLINE: 90266454.

FRASER M., HILL D.F., MERCER A.A.,

VIROLOGY 176:379-389(1990).

EMBL: M30023; G332564; -
 SEQUENCE FROM N.A.
STRAIN=H37RV;
TYAGI J.S.;
 MYCOBACTERIUM TUBERCULOSIS.
PROKARYOTA; FIRMICUTES; ACTINOMYCETALES; MYCOBACTERIACEAE
 SEQUENCE FROM N.A.
STRAIN-H37RV;
 PREDICTED ORF
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 STRAIN-H37RV;
 SUBMITTED (DEC-1991)
 SEQUENCE FROM N.A.
 PARAPOXVIRUSES.
 VIRIDAE; DS-DNA ENVELOPED VIRUSES;
 296
 Match 10.1%;
Local Similarity 25.4%;
les 16; Conservative
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 Local Similarity
nes 24; Conser
 67
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 YPR 69
 PIMTILQAPTPAPSTIPGPRRGSGPEIFTFDP-LPEPAAAPAGRPSA-SRGHRKRSRRVL
 ROORAHORRRGRR
 QAPTPAPSTIPGPRRGSGPEIFTFDPLPE-PAAAPAGRPSASRGHRKRSRRVLYPRV-VR 72
 QPRRRAPRAAGARRGRGPAPRQQQRQPRVQRAAAAQRRAQQRRQRQPPRRVRARRARAR 295
 YRR 70
 PSQPALPPRPPTPPAVPNPPNPPAPPLDNSSPRLPTAPPSPPRKPNPPAPARRRRTAALR 67
 RQLPVEEPNPAKR
 DASGUPTA N., AGGARWAL A.N., PANDE J
BIOCHEM. BIOPHYS. 32:429-436(1995).
 115
 351 AA;
 10.2%;
llarity 32.9%;
Conservative
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 PRELIMINARY;
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 12106 MW;
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 Score 112; DB 9;
Pred. No. 3.65e-02;
23; Mismatches 22
 Score 114; DB 11;
Pred. No. 2.07e-02;
12; Mismatches 35
 PRT;
 PRT;
 AF306566 CRC32;
 8EEF741B CRC32;
 POXVIRIDAE; CHORDOPOXVIRINAE;
 ROBINSON A.J.;
 285
 115
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 Q65553;
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Q1-NOV-1996
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Q1-JAN-1998
 STRAIN-JURA;
SCHWYZER M., STYGER D., VOGT B.,
LABOISSIERE S., MISRA V., VLCEK
VET. MICROBIOL. 53:67-77(1996).
 STRAIN-COOPER;
SCHWYZER M., STGER D., VOGT B., LOV
SCHWYZER M., VICEK C.,
LABDISSIERE S., MISRA V., VLCEK C.,
VET. MICROBIOL. 0:0-0(1996).
 SCHWYZER M., VLCEK C., LOWERY D.E., THIRY E., PACES V.; SUBMITTED (AUG-1996) TO EMBL/GENBANI
 BOVINE HERPESVIRUS TYPE 1.
VIRIDAE; DS-DNA ENVELOPED VIRUSES; HERPESVIRIDAE; ALPHAHERPESVIRINAE
 P78977;
01-MAY-1997 (TREMBLREL. 03,
01-MAY-1997 (TREMBLREL. 03,
01-JAN-1998 (TREMBLREL. 05,
 SEQUENCE FROM N.A.
STRAIN-JURA;
 SEQUENCE OF 1-179 FROM N.A.
 SUBMITTED (AUG-1996) TO
 SCHWYZER M.
 STRAIN-COOPER;
 SEQUENCE FROM N.A.
 SEQUENCE OF 1-179 FROM
 STRAIN-COOPER;
 MEDLINE; 97127825.

RAMON A., GIL R., BURGAL M., YEAST 12:1535-1548(1996).

EMBL; Z81006; E274837; -.
 CELL WALL PROTEIN PRECURSOR.
YARROWIA LIPOLYTICA (CANDIDA LIPOLYTICA).
EUKARYOTA; FUNGI; ASCOMYCOTINA; HEMIASCOMYCETES
 SEQUENCE FROM N.A.
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 SIGNAL.
 SEQUENCE FROM N.A.
STRAIN=CX39-74A; TISSUE-PINA240;
 118
 122 ICHTKTVTLSTEVTLTPTPVPQTTTPAVEPKPTPEVPEVKPEPTPEV-PGVKPEPTRGPP 180
 239
 181
 60
 H
 ASLAP-TP-VSPVLEPFNLTSEPSDYALDLS 146
 LSLPPRSPRSSPSLPPLSRPTLPPTSRL-LS 268
 APKPEPEVPEVKPEPTPEVPEVRPEPTPAPLPPRPSL-RSLRSSPSLPPLPLPPSPSP-S
 MCHSRSCHPTMTILQAPTPAP-STIPGPRRGSGPEIFTFDPLPEPAAAPAGRPSASRGHR 59
 KRSRRVLYPRVVRRQLP-VEEPNPAKRLLFLLLTIVFCQILMAEEGVPA-PLPPEDAPNA 117
 Similarity
 1
17
285 AA;
 (TREMBLREL. 01, (TREMBLREL. 01, TREMBLREL. 05,
 STYGER D., VOGT B.;
S., MISRA V., VLCEK
 10.1%;
larity 28.5%;
Conservative
 VLCEK
 PRELIMINARY;
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LOWERY D.E.,
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 084630

084630;

01-NOV-1996 (TREMBLREL 01,

01-NOV-1996 (TREMBLREL 01,

01-NOV-1996 (TREMBLREL 01,
 EMBL;
 MEDLINE; 95201245.
 MEDLINE; 95133167.

LU Z., LI Y., ZHANG Y., KUT:

VIROLOGY 206:339-352(1995).

EMBL; U42580; G11814'9; -.

SEQUENCE 225 AA; 25053 M
 GENOME,
 2705 PITVLVPAPVPAPAPTPAPAPTPAPAPTPAPPLPPPAPDGAMGALSATRRPTRRAGARKS 2764
 SUBMITTED (SEP-1997) TO E EMBL; Z78205; E258467; -. EMBL; AJ004801; E1187307; SEQUENCE 3247 AA; 3321
 EUKARYOTA; PLANTA;
 VIRIDAE;
 PARAMECIUM BURSARIA CHLORELLA VIRUS 1
 SCHWYZER M.;
 SEQUENCE FROM N.A
 SIGNAL;
 ABRAHAMS S., HAYES C.M., WATSON J. PLANT MOL. BIOL. 27:513-528(1995). EMBL; L36120; G535586; -.
 SEQUENCE FROM N.A. STRAIN-CV. SIRIVER
 FABACEAE.
 SEQUENCE FROM N.A.
 SUBMITTED (NOV-1997)
 149 HDLP 152
 73
 16
 66
 90 APKPAPKPVPRPKPAPKPVP-KPKPKPAPKPAPKPVFLGRPKKNRPRTTGLFVFVSVW 148
 Local Similarity
 Local
 ø
 RQLP
 LYPRVVRRQ 74
 L-PAAQPRQ 2772
 PTMTILQAPTPAPSTIPGPRRGSGPEIFTFDPLPEPAAAPA-GRPSASRGHRKRS--RRV 65
 APTPAPSTIPGPRRGSGPEIFTFDPLPEPAAAPAGRPS-ASRGHRKRSRRV-LYPRV-VR 72
 Similarity 35.9%;
23; Conservative
 PARTIAL
 STRUCTURAL PROTEIN.
 DS-DNA NONENVELOPED VIRUSES;
 Conservative
 EMBRYOPHYTA;
 9.98;
 10.0%;
 25053 MW;
 TISSUE-STEM
 332189
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 KUTISH G.F.,
 EMBL/GENBANK/DDBJ
 EMBL/GENBANK/DDBJ DATA BANKS.
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 Score 110; DB 11; 1
Pred. No. 6.41e-02;
14; Mismatches 23;
 Pred.
11; 1
 MW.
 LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
 CREATED
 Score 111; DB 11;
Pred. No. 4.84e-02;
 PRT;
 PRT;
 27D5CD5E CRC32;
 ANGIOSPERMAE;
 SEQUENCE UPDATE)
ANNOTATION UPDATE)
 Mismatches
 0353E339 CRC32;
 228
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 225
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PHYCODNAVIRIDAE
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 WILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M.,
BONFIELD J., BURTON J., CONNELL M., COPSEY T., COOPER J.,
COULSON A., CRAXTON M., DEAR S., DU Z., DURBIN R., FAVELLO A.,
COULSON A., CRAXTON M., DEAR S., DU Z., DURBIN R., FAVELLO A.,
COULTON L., GARRONER A., GREEN P., HAWKINS T., HILLER L., JIER M.
JOHNSTON L., JONES M., KERSHAW J., KIRSTEN J., LAISTER N.,
LATREILLE P., LIGHTNING J., LLOYD C., MCMURRAY A., MORTIMORE B.,
O'CALLAGHAN M., PARSONS J., PERCY C., RIFKEN L., ROOPRA A.,
SAUNDERS D., SHOWNKEEN R., SMALDON N., SMITH A., SONNHAMMER E.,
STADEN R., SULSTON J., THIERRY-MIEG J., THOMAS K., VAUDIN M.,
VAUGHAN K., WATERSTON R., WATSON A., WEINSTOCK L.,
 001662;
01-JUL-1997 (TREMBLREL. 04, CREATED)
01-JUL-1997 (TREMBLREL. 04, LAST SEQUENCE UPDATE)
01-JUL-1997 (TREMBLREL. 04, LAST ANNOTATION UPDATE)
01-JULAR TO CUTICULAR COLLAGEN.
 096343;
01-FEB-1997 (TREMBLREL. 02, CREATED)
01-FEB-1997 (TREMBLREL. 02, LAST SEQUENCE UPDATE)
01-FEB-1997 (TREMBLREL. 02, LAST ANNOTATION UPDATE)
MIROSINASE-BINDING PROTEIN RELATED PROTEIN (FRAGMENT).
 SEQUENCE FROM N.A.
STRAIR-20516 OF SVALOFS KARAT;
TAIPALENSUU J., FALK A., EK B., RASK L.;
SUBMITTED (NOV-1996) TO EMBL/GENBANK/DDBJ DATA BANKS EMBL; U59446; G1655830; -...
NON_TER 1 1
 STRAIN-BRISTOL N2;
MEDLINE; 94150718.
 CAENORHABDITIS
 001662
 BRASSICA NAPUS (RAPE).
EUKARYOTA; PLANTA; EMB
 Q96343
 SEQUENCE FROM N.A.
 EUKARYOTA;
 T28F2.6.
 SEQUENCE
 CAPPARALES;
 295 LRTPAPAPSPAPGPAPAPAPASHP-APAPAPAPAPAPGQGPRPAPAPG 339
 135 TSEPS 139
 154
 Local Similarity
hes 20; Conser
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 LQAPTPAPSTIPGPRRGSGPEIFTFDPLPEPAAAPA-G-RPSASRG
 SSPPA 158
 APTPAPSTIPGPRRGSGPEIFTFDPLPEPAAAPAGRPSASRGHRKRSRRVLYPRVVRRQL
 PVEEPNPAKRILFILITIVFCQILMAEEGVPAPI-PPEDAPNAASLAPTPVSPVLEPFNL
 PVQQSPPPTPLTPPPVQST-PPPASPPPASPPPFSPPPATPPPATPPPATPPPALTPTPL
 Similarity
30; Conser
 METAZOA;
 228
 552 AA; 59270 MW;
 CRUCIFERAE.
 Conservative
 Conservative
 ELEGANS
 AA;
 PRELIMINARY;
 PRELIMINARY;
 9.7%;
 9.98;
 228
22480
 EMBRYOPHYTA; ANGIOSPERMAE;
 ACOELOMATES; NEMATODA; SECERNENTEA; RHABDITIDA
 WOHLDMAN P.;
 MW;
 Score 110; DB 8;
Pred. No. 6.41e-02;
36; Mismatches 56
 Score 108; DB 8;
Pred. No. 1.12e-01;
 11; Mismatches
 PROLINE RICH PROTEIN.
2A2B03B9 CRC32;
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 6861EF25 CRC32;
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 DICOTYLEDONEAE;
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Q1-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPI

Q1-MAY-1997 (TREMBLREL. 03, LAST ANNOTATION

TOTAL VIRUS GENE F12L HOMOLOG.
 027212
027212;
027212;
01-NOV-1996
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01-NOV-1996
 ARTICULIN P60.
PSEUDOMICROTHORAX DUBIUS
 J. CELL BIOL. 130:1401-1412(1995).
EMBL; L41557; G767685; -.
 SEQUENCE FROM N.A.
 EUKARYOTA; MITOCHONDRIAL
 SEQUENCE FROM N.A.
STRAIN-BRISTOL N2;
 STRAIN-BRISTOL N2;
MADSEN C., FRONICK B.
SUBMITTED (APR-1997)
 SEQUENCE FROM N.A.
 SEQUENCE FROM STRAIN-NZ2;
 SEQUENCE
 HUTTENLAUCH I.,
 STRAIN-N5B
 NASSULIDA.
 SEQUENCE FROM N.A
 SUBMITTED (OCT-1995)
 MERCER
 PARAPOXVIRUSES
 NATURE 368:32-38(1994).
 363 AAAGAAAPPPAAAAAAPEPAP-APAAAPPPAAAGGSPTGGYRRKKVRRVL--RIVR 417
 391 HVPIPHPVPVAQEVIVQQPFAVPQPYTVQQEVPIPHPVPVPQPYAVP-QPVPVPTPVAVP
 332 VNVPVDVPIEVPVDRDVPVPFQLN-IDVPVDVPVARPVPVERIIQQPIPLEQPRLVEQ
 Local Similarity
nes 22; Conser
 74 QLPVEEPNPAKRLLFLLLTIVFCQILMAEEGVPAPLP-PEDAPNAASLAPTPV-SPVLEP
 14
 Local Similarity
les 30; Conser
 16 APTPAPSTIPGPRRGSGPEIFTFDPLPEPAAAPAGRPSASRG-HRKRSRRVLYPRVVR 72
 LQAPTPAPSTIPGPRRGSGPEIFTFDPLPEPAAAPAGRPSASRGHRKRSRRVLYPRVVRR
 A.A.;
 96032269.
JCH I., GEISLER N.,
 568 AA;
 9.2%;
llarity 25.0%;
Conservative
 (TREMBLREL.
 (TREMBLREL.
 9.2%; Score 102; DB 3; Locality 37.9%; Pred. No. 5.74e-01; Conservative 17; Mismatches 15;
 PRELIMINARY;
 ENVELOPED
 61110 MW; CA5BB376 CRC32;
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 EMBL/GENBANK/DDBJ DATA BANKS
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 EUKARYOTES;
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LAST ANNOTATION UPDATE)
 Score 102; DB 3;
Pred. No. 5.74e-01;
24; Mismatches 62
 PLESSMANN
 25B7D236 CRC32;
 POXVIRIDAE; CHORDOPOXVIRINAE;
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STRAIN=DSM43798;
MEDLINE; 92162190.
HEINNINGSEN M., ROG
 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
01-NOV-1996 (TREMBLREL. 01, LAST ANNOTATION UPDATE)
SIALIDASE (EC 3.2.1.18) (EXO-ALPHA-SIALIDASE) (NEURAMINIDASE)
(N-ACYLNEURAMINATE GLYCOHYDROLASE) (ALPHA-NEURAMINIDASE).
NANH
 STRAIN-DSM43798;
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 ACTINOMYCES VISCOSUS. PROKARYOTA; FIRMICUTES;
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DE MC018L.
GN MCLUSCUM COI
OC VIRIDAE; DS-0
OC VIRIDAE; DS-0
OC VIRIDAE; DS-1
OC WOLLUSCUPOXV
RN [1]
RP SEQUENCE FROI
RA MOSS B;
RL SCIENCE 273:1
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VIRUS GENES 11:21-29(1995).
EMBL; U34774; G1002997; -.
EMBL; S82833; G1754760; -.
SEQUENCE 640 AA; 70097 MW;
 SUBMITTED (JUN-1996) TO EMBL/GENBANK/DDBJ DATA EMBL; U60315; G1491961; -. SEQUENCE 680 AA; 72398 MW; 43AB9271 CRC32;
 SEQUENCE FROM N.A.
SENKEVICH T.G., BUGERT J.J.,
 SEQUENCE FROM N.A SENKEVICH T.G., BU
 MOLLUSCUM CONTAGIOSUM VIRUS VIRIDAE; DS-DNA ENVELOPED V.
 SCIENCE 273:813-816(1996).
 MOLLUSCIPOXVIRUSES
 SKRVR-ARAVR-QLP 289
 RSRRVLYP-RVVRRQL-PVEEPNPAKRLLFLLTIVFCQILMAEEG-VPAPLPPED 113
 RCFRLAYPLREVASQLYPVGKPRMVSKLTRGLLAIALCEVTRSAEVKIPVLFDPAD 491
 9.2%;
Similarity 36.0%;
27; Conservation
 9.2%;
Similarity 35.7%;
20; Conservation
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(TREMBLREL.)
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 BUGERT J.J.,
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02,
 US SUBTYPE 1 (MCVI).
VIRUSES; POXVIRIDAE; CHORDOPOXVIRINAE;
 Score 102; DB 11;
Pred. No. 5.74e-01;
19; Mismatches 23
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 Score 102; DB 11;
Pred. No. 5.74e-01
9; Mismatches 2
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O1-JAN-1998 (TREMBLREL
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O5, LAST ANQUENCE UPDATE)
ENDOGLUCANASE A (EC 3.2.1.4) (ENDO-1,4-BETA-GLUCANASE A)
CCELLULASE A).
 BIOL. CHEM. HOPPE-SEYLER 372:1065-1072(1991).

-I- CATALYTIC ACTIVITY: HYDROLYSIS OF 2,3-2,6- AND 2,8-GLYCOSIDIC CATALYTIC ACTIVITY: HYDROLYSIS OF 2,3-2,6- AND 2,8-GLYCOSIDIC LINKAGES JOINING TERMINAL NON-REDUCING N- OR O-ACYLATED RESIDUES TO GALACTOSE, N-ACETYLHEXOSAMINE, OR N- OR O-ACYLATED NEURAMINYL RESIDUES IN OLIGOSACCHARIDES, GLYCOPROTEINS,
 NON_TER
 ANAEROCELLUM THERMOPHILUM.

EUBACTERIA; FIRMICUTES; LOW G+C GRAM-POSITIVE BACTERIA;

CLOSTRIDIACEAE; CELLULOLYTIC THERMOPHILE GROUP; ANAEROCELLUM.
 GLYCOLIPIDS OR COLOMINIC ACID. EMBL; X62276; G39255; -.
 SEQUENCE FROM N.A. STRAIN=Z-1320;
 SEQUENCE
 PROSITE; PS00592; GLYCOSYL_HYDROL_F9_1; 1.
PROSITE; PS00698; GLYCOSYL_HYDROL_F9_2; 1.
CELLULOSE DEGRADATION; HYDROLASE; GLYCOSIDASE; SIGNAL; REPEAT
 EMBL; 286105; E350354;
 :-
 ZVERLOV V.;
 HYDROLASE;
 874 RAADPGP
 816 SPAPSRNAAPTPKPGMEPDEID-RPSDGTMAQPTGAP-ARRVPRRRRRRPAAGCLARDQ 873
 630 PTPTVTPTPTPTPTSTATPTPTPTPTV-TPTPTPTPTATPTSTPTPT 675
 16 APTPAPSTIPGPRRGSGPEIFTFDPLPEPAAAPAGRPSASRGHRKRSRRVLYPRVVRRQL 75
 76 PVEEPNP 82
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 (FAMILY 9 OF GLYCOSYL HYDROLASES).
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(FAMILY 48 OF GLYCOSYL HYDROLASES).
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 h 9.2%;
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913 AA; 962
 1711 AA;
 9.2%;
larity 29.9%;
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 96216 MW;
 189979 MW; 475389DE CRC32;
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LAST ANNOTATION UPDATE)
 Score 103; DB 9; Le
Pred. No. 4.39e-01;
15; Mismatches 15;
 Score 103; DB 9;
Pred. No. 4.39e-01;
14; Mismatches 31
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 J. BIOL. CHEM. 271:22624-22634(1996).
-I- SUBCELLULAR LOCATION: NUCLEAR (BY SEMBL; U45665; G1518932;
-MGD; MGI:107321; CUTL2.
PROSITE; PS00027; HOMEOBOX_1; 1.
HOMEOBOX; DNA-BINDING; NUCLEAR PROTEIN.
SEQUENCE 1426 AA; 154703 MW; 478F57
 CUTL2.
MUS MUSCULUS (MOUSE).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; RODENTIA.
 QUAGGIN S.E., VANDEN HEUVEL G.B., GOLDEN K.,
J. BIOL. CHEM. 271:22624-22634(1996).
-I- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILA)
 SEQUENCE FROM N.A.
 370 LGTEPPYPPQLPPPPGPEDP-LSPSPAQPLLGP-SLGPDGPRNFSL 413
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 LMAEEGVPAPLPPEDAPNAASLAPTPVSPVLEPFNLTSE-PSDYAL 143
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llarity 34.8%;
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Search completed: Fri Apr 17 13:39:48 1998 Job time : 47 secs.

|            | T49532 ya76f12.sl Homo sapien 0<br>AA301628 EST14813 Aorta endothe 0                                                                            | 14 345 28.1 40<br>15 332 27.0 41                                                   |
|------------|-------------------------------------------------------------------------------------------------------------------------------------------------|------------------------------------------------------------------------------------|
| -          | zc35b02.sl Soares<br>zk74a02.sl Soares                                                                                                          | c 12 368 30.0 375<br>c 13 351 28.6 355                                             |
| -          | N29782 yw91h09.51 Homo sapien 0                                                                                                                 | 10 376 30.6 39<br>11 373 30.4 44                                                   |
|            | AA034911 zk25c01.s1 Soares preg 0 W52269 zc46a10.s1 Soares sene 0                                                                               | 402 32.7 48<br>383 31.2 41                                                         |
|            | W52268 zc46al0.rl Soares sene 0                                                                                                                 | 406 33.1 44                                                                        |
|            | AA043722 zk59bll.sl Soares preg 0                                                                                                               | 420 34.2 46                                                                        |
|            | AA047094 zk74a02.rl Soares preg                                                                                                                 | 3 448 36.5 47<br>4 422 34.4 42                                                     |
|            | N32077 yw97d08.sl Homo sapien 0.<br>W60982 zc98h09.sl Pancreatic 0.                                                                             | 495 40.3 55<br>450 36.6 45                                                         |
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|            | ; Variance                                                                                                                                      | cistics: Mean 11.559                                                               |
|            | 10:gb_est2 11:gb_est3 12:gb_est4 13:gb_est5<br>6 15:gb_est7 16:gb_est8 17:gb_est9 18:gb_est10<br>11 20:gb_sts 21:gb_gss 22:gb_est12 23:gb_est13 | 9:gb<br>14:g<br>19:g                                                               |
| So         | 7:em_est8 8:em_gss                                                                                                                              | f:em_est6<br>Database: genbank-est                                                 |
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| n          | lt                                                                                                                                              | Scoring table: TABLE default                                                       |
|            | ATGTGTCACTCTCGCAGCTGAAAAAAAAAAAAAA                                                                                                              | quence: 1                                                                          |
| a          | 9-910-9<br>from US08799910.seq                                                                                                                  | Title: >US-08-799<br>Description: (1-1228) fi<br>Perfect Score: 1228               |
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|            | n F. Collins, Blocomputing Research Unit.<br>-1997 University of Edinburgh, U.K.<br>on rights by Oxford Molecular Ltd                           | Release 3.0.4A John 1<br>Copyright (c) 1993–19<br>Distribution                     |
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| C06218<br>HUM4S125   |                                                 |      | AA073253 | W71619        |               |              |                  | W77628          | HSAAACM | AA03497     | AA450645        | AA35694   | AA00368       | AA04342   | AA2768  |           |         |               | AA372        | H8007         | AA431     | T4953         | N4539   | N2591   |                | W4522       | N2507                  |
| hro                  | yx76g03.rl Homo sapien<br>Human HL60 3'directed | Sur  | Stratag  | rl Soares mou | sl Soares tes | lomo sapiens | 23c12.rl Barstea | 68a09.rl Soares | sapiens | 3.rl Soares | 1.rl Soares mou | Jurkat T- | rl Soares mou | rl Soares | rl Soar | rl Homo s | rl Soar | rl Homo sapie | Colon adenoc | sl Homo sapie | rl Soares | rl Homo sapie | rl Home | s1 Homo | 0b07.rl Pancre | sl Pancreat | yw40f06.sl Homo sapien |
| 2.10e-27<br>6.39e-11 | .346                                            | .75€ | . 886    | 30e           | . 986         | . 146        | . 106            | . 236           | . 786   | .976        | . 156           | . 496     | 656           | . 656     | . 956   | . 686     | .67     | . 306         | .00          | 00            | 00        | .00           | .006    | 00      | .00e+          | 0.00e+      | O                      |

## ALIGNMENTS

|                                                                                                                                                                                                                                            | COMMENT | TITLE<br>JOURNAL                                  |                                                                                                                                                                                  | AUTHORS                                                         | REFERENCE          |                                                                                                                                                                                                  |                                                       | ORGANISM                                                           |                                                                                                                              |                                                              |                                                                  |                                                                  |                                                                | SOURCE                                                            | NID        | RESULT 1 LOCUS DEFINITION ACCESSION                                           |
|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|---------|---------------------------------------------------|----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|-----------------------------------------------------------------|--------------------|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|-------------------------------------------------------|--------------------------------------------------------------------|------------------------------------------------------------------------------------------------------------------------------|--------------------------------------------------------------|------------------------------------------------------------------|------------------------------------------------------------------|----------------------------------------------------------------|-------------------------------------------------------------------|------------|-------------------------------------------------------------------------------|
| Washington University School of Medicine Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286 1800 Fax: 314 286 1810 Email: est@watson.wustl.edu High quality sequence stops: 416 |         | The WashU-Merck EST Project<br>Unpublished (1995) | Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and | Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., | 1 (bases 1 to 553) | peuterostomita; chordata; verteorata; unathostomata; osteronnyes;<br>Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria;<br>Entheria: Archonta: Primates: Catarrhini: Hominidae: Homo | Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata; | constructed by Bento Soares and M. Fatima Bonaldo.<br>Homo sapiens | (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT7T3 vector (Pharmacia). Welbrary | Oligo(d) primer [5'-TGTTACCAATCTGAAGTGGGAAGCGGCCGCGATTTTTTTT | weeks post conception. 1st strand cDNA was primed with a Not I - | Rsite2=Eco RI two placentae: one from 8 weeks and another from 9 | 8to9weeks 2NbHP8to9W vector-pT7T3D (Pharmacia) with a modified | human clone=260175 primer=m13 -40 forward library=Soares placenta | 91152476 . | N32077 553 bp mRNA<br>yw97d08.s1 Homo sapiens cDNA clone 260175 3'.<br>N32077 |

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 CGTGACAGCCCAACCCCAACCCTCTACCTCGCAGCCACCCTAAAGGCGACTTCAAG
 GACAGTAAATCAATTTTATTTGTGTTCACAGAACATACTAGGCGATGTCGATAGTCGCTC
 ACTICATCCCAGCCGGGACGTCCTCCCCCACCCGAGTCCTCCCCATTTCTTCTCCTACTI
 CGTGACAGCCCACCAACCCCAACCCTCTACCTCGCAGCCACCCTAAAAGGCGACTTCAAG 124
 GACAGTAAATCAATTTTATTTGTGTTCACAGAACATACTAGGCGATCTCGACAGTCGCTC
 AAG--GAATTAAATTAACGACGCTTTTCCTTCNCACGGGGCCTAGGCCCAGCTGGGNTGT 542
 GTACACATCTCCATCACCTAGGAGGACGTACATTAATACATATAAAATATTAGGGAGCAAT
 ACCTGCATTTACAGCAGGGGAACATCTCACACCCTTGCATAAGTTAAAATAATAATATAC
 GCCTCGGT
 AATAAGAAATAAATTAACGACGCTCT
 g1367741
EST.
 Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Location/Qualifiers
Eukaryotae: mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 459)
Hiller, L. Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Tan, F., Trevaskis, E., Waterston, R., Williamson, A., Wohldmann, P. and Wilson, R. washU-Merck EST Project
Unpublished (1995)
 zc98h09.s1
w60982
 W60982
 Homo sapiens
 Similarity
 human.
 40.3%;
llarity 96.4%;
Conservative
 /organism="Homo sapiens"
/clone="260175"
<1. .>553
 459 bp
Pancreatic
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165 c
 Score 495; DB 12;
Pred. No. 0.00e+00;
 106
 mRNA
Islet Homo
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 -CCTTCCCACCGGGCCTAGCCCCAGCTGGGCTGT
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AA047094
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 Email: est@watson.wustl.edu
This clone is available royalty-free through
IMAGE Consortium (info@image.llnl.gov) for fu
Seq primer: ETPrimer
 Contact: Wilson RK
WashUnMerck EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. I
Tel: 314 286 1800
Fax: 314 286 1810
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 858 TTGAGCTTTGTGGGACTGGTGGAAGCAGGACACCTGGAACTGCGGCAAAGTAGGAGAAGA 917
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 Contact: Wilson RK
WashU-Merck EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis,
 Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Hom 1 (bases 1 to 470)
Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra, Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and Marcaskis,E., Waterston,R., Williamson,A., Wohldmann,P.
 High quality sequence stop: 358. Location/Qualifiers
 The WashU-Merck EST Unpublished (1995)
 Homo sapiens
 Tel: 314 286 1800
Fax: 314 286 1810
 Eukaryotae;
 103
 est@watson.wustl.edu
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Eutheria; Primates; Catarrhini; Hominidae; F
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Pred. No. 0.00e+00;
0; Mismatches 9;
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 TITLE
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 1038 ACTTCGGCGGACCATTAGGAATGAGATCCGTGAGATCCTTCCATCTTCTTGAAGTCGCCT
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 AGATCGCCTAGTATGTTCTGTGAACACAAATAAAATTGATTTACTG
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Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Theising,B.,
White,Y., Wylie,T., Waterston,R. and Wilson,R.
WashU-Merck EST Project 1997
Unpublished (1997)
 WashU-Merck EST Project
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4444 Forest Park Parkway,
Tel: 314 286 1810
Fax: 314 286 1810
 Homo sapiens
Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Ho
 This clone is available royalty-free through LLNL; MAGE Consortium (info@image.llnl.gov) for further: Seg primer: -41ml3 fwd. ET from Amersham High quality sequence stop: 374.
 Email: est@watson.wustl.edu
 Contact: Wilson RK
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 School of Medicine way, Box 8501, St. Louis,
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tumor
 EST 06-JUN-1997
NbHOT Homo sapiens cDNA clone 810724
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 Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL;
IMAGE Consortium (info@image.llnl.gov) for further
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 Tel: 314 286 1800
Fax: 314 286 1810
 Washington University Scho
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 WashU-Merck EST Project
 Homo sapiens
 WashU-Merck EST Project
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 mitochondrial eukaryotes; Metazoa; Chordata; Mammalia; Eutheria; Primates; Catarrhini; Ho
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Unpublished (1997)
Washington University
 Contact: Wilson RK WashU-Merck EST Pro
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Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Ho
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Pred. No. 0.00e+00;
0; Mismatches 3
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Tel: 314 286 1800

Fax: 314 286 1810

Email: estewatson.wustl.edu

This clone is available royalty-free through LLNL; con

IMAGE Consortium (info@image.llnl.gov) for further info
Seq primer: -26m13 rev2 ET from Amersham

Location/Qualifiers

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The sequence stop: 369.

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 GGCGCCACCCCTGTGTCCCCCGTCCTCGAGCCCTTTAATCTGACTTCGGAGCCCTCGGA 421
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W52268 447 bp mRNA EST 11-OCT-1996 zc46a10.rl Soares senescent fibroblasts NbHSF Homo sapiens cDNA clone 325338 5' similar to SW:GL96_MOUSE P46694 IMMEDIATE EARLY PROTEIN GLY96. [1] ;.
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Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M.
Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marr
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Trevaskis, E., Waterston, R., Williamson, A., Wohldmann, P.
 WashU-Merck EST Project
Washington University Scho
4444 Forest Park Parkway,
 This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Insert Length: 3171 Std Error: 0.00
 Tel: 314 286 1800
Fax: 314 286 1810
 Contact: Wilson RK
 Unpublished (1995)
 The WashU-Merck EST
 g1349380
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 School of Medicine way, Box 8501, St. 1
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 WashIngton University School of Medicine 4444 Forest Park Parkway, Box 8501, St. J
 Tel: 314 286 1800
Fax: 314 286 1810
 Contact: Wilson
 Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Ho
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 ACTTCATC ---C-CAGCC-GGGACGTCCTCCCCACCGAGTCCTCCCCATTTCTTCTC
 TALL TO THE TRANSPORT T
 Contact: Wilson RK
WashU Merck EST Project
Washington University School o
4444 Forest Park Parkway, Box
 Hiller,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,Q., Marra, Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. an
 Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; H (bases 1 to 413)
 Seq primer: mob.REGA+ET
 Tel: 314 286 1800
Fax: 314 286 1810
 Unpublished
 The WashU-Merck EST
 Wilson, R.
 Homo sapiens
 human.
Location/Qualifiers
 (1995)
 Project
 School of Medicine way, Box 8501, St. 1
 A EST 1
fibroblasts NbHSF Homo
 e,M., Lennon,O., Marra,M.
Soares,M., Tan,F.,
 Louis,
 Wohldmann, P. and
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 63108
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 Ното
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 1145
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BASE COUNT
ORIGIN
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Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M.,
 Homo sapiens
Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata;
 constructed by Bento Soares and M. Fatima Bonaldo
 110
 Conservative
 QJ
 3'], double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT77 vector (Pharmacia). Library went through one round of normalization to a Cot = 5. Library constructed by Bento Soares and M.Fattima Bonaldo."
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0; Mismatches 1
 1. .>413)
77 °
 89 t
 1 others
 Indels
 NbHSF"
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 Osteichthyes;
 Gaps
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JOURNAL
 Query Match
Best Local :
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Homo sapiens
Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Ho;
1 (bases 1 to 443)
1 (bases 1 to 643)
Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.
Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra
Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
 W47587
g1332247
 Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Location/Qualifiers
 Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and Wilson,R.
 W47587 443 bp mRNA EST 11-OCT-19 zc35b02.rl Soares senescent fibroblasts NDHSF Homo sapiens clone 324267 5' similar to SW:GL96_MOUSE P46694 IMMEDIATE PROTEIN GLY96. [1] ;.
 The WashU-Merck EST Unpublished (1995)
 Contact: Wilson
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 Length 390;
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 Marra, M.,
 Homo.
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 304
 64
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